

43540

Delavai, Jan

---

**From:** Roark, Jessica  
**Sent:** Wednesday, May 30, 2001 4:39 PM  
**To:** Delavai, Jan  
**Subject:** 09/509,283

Jan,

Please search, including interference,

SEQ ID NO:2  
SEQ ID NO:2 as an oligo search

Results on paper and disk please.

Thanks!

*Jessica H. Roark*

CM1 9B03  
Mailbox 9E12  
Art Unit 1644  
703 605-1209

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:03 ; Search time 19.73 Seconds

(Without alignments)  
573.660 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078

Sequence: 1 MKSGLMYFFFLCRLRVLTG.....YMEKRAVNTAKKSLIDVTL 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq 0401.\*

- 1: /SID56/gcgdata/geneSeq/geneSeq/AA1980.DAT.\*
- 2: /SID56/gcgdata/geneSeq/geneSeq/AA1981.DAT.\*
- 3: /SID56/gcgdata/geneSeq/geneSeq/AA1982.DAT.\*
- 4: /SID56/gcgdata/geneSeq/geneSeq/AA1983.DAT.\*
- 5: /SID56/gcgdata/geneSeq/geneSeq/AA1984.DAT.\*
- 6: /SID56/gcgdata/geneSeq/geneSeq/AA1985.DAT.\*
- 7: /SID56/gcgdata/geneSeq/geneSeq/AA1986.DAT.\*
- 8: /SID56/gcgdata/geneSeq/geneSeq/AA1987.DAT.\*
- 9: /SID56/gcgdata/geneSeq/geneSeq/AA1988.DAT.\*
- 10: /SID56/gcgdata/geneSeq/geneSeq/AA1989.DAT.\*
- 11: /SID56/gcgdata/geneSeq/geneSeq/AA1990.DAT.\*
- 12: /SID56/gcgdata/geneSeq/geneSeq/AA1991.DAT.\*
- 13: /SID56/gcgdata/geneSeq/geneSeq/AA1992.DAT.\*
- 14: /SID56/gcgdata/geneSeq/geneSeq/AA1993.DAT.\*
- 15: /SID56/gcgdata/geneSeq/geneSeq/AA1994.DAT.\*
- 16: /SID56/gcgdata/geneSeq/geneSeq/AA1995.DAT.\*
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- 18: /SID56/gcgdata/geneSeq/geneSeq/AA1997.DAT.\*
- 19: /SID56/gcgdata/geneSeq/geneSeq/AA1998.DAT.\*
- 20: /SID56/gcgdata/geneSeq/geneSeq/AA1999.DAT.\*
- 21: /SID56/gcgdata/geneSeq/geneSeq/AA2000.DAT.\*
- 22: /SID56/gcgdata/geneSeq/geneSeq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067.5	99.0	199	19	W75956
2	1067.5	99.0	199	19	W75957
3	1067.5	99.0	199	20	W75958
4	1067.5	99.0	199	21	W75959
5	1052	97.6	198	21	Y92213
6	727	67.4	200	21	Y92212
7	723.5	67.1	200	21	B08723
8	712	66.0	200	19	W75958
9	695.5	64.5	200	19	W71874
10	690.5	64.1	216	19	W71875
11	143	13.3	225	20	Y41136

12	141	13.1	221	21	Y32286	Feline CD28, Feli
13	141	13.1	221	21	Y32279	Cat CD28 receptor.
14	136	12.6	220	13	R20805	Human CD28 antigen
15	136	12.6	220	13	R27103	Sequence encoded b
16	136	12.6	220	17	W02131	Human CD28 cDNA pr
17	136	12.6	220	17	R91433	Human CD28 antigen
18	136	12.6	220	18	M38413	CD28. Homo sapien
19	136	12.6	220	19	W80442	Human CD28 antigen
20	136	12.6	220	21	Y69128	Human cell surface
21	136	12.6	220	21	Y44294	Human CD28 recepto
22	129.5	12.0	225	20	Y41135	Mouse CD28 protein
23	129.5	11.3	223	20	Y41137	Human CD28 protein
24	120.5	11.2	367	18	W35862	Human CD28:19g2a c
25	119.5	11.1	152	16	R67706	Human CD28 for use
26	119.5	11.1	152	16	R67706	CD28 extracellular
27	119.5	11.1	117	20	Y24469	Human CD28 gene pr
28	89.5	8.3	117	20	Y24469	Mouse dephosphoryl
29	86	8.0	635	20	Y24321	Mouse dephosphoryl
30	86	8.0	663	20	Y24322	Soluble human CTLA
31	85.5	7.9	223	18	W25111	Soluble human CTLA
32	85	7.9	187	19	W29728	Chicken CD28 prote
33	84.5	7.8	226	20	Y41138	HIV fusion protein
34	84	7.8	229	11	R04495	Human CTLA-4 prote
35	83.5	7.7	223	21	Y15129	Human secreted pro
36	83	7.7	209	21	Y94998	Sequence of mouse
37	81.5	7.6	330	8	P70445	Human T cell speci
38	81	7.5	187	17	R86945	CTLA4 receptor wit
39	81	7.5	187	20	Y41130	Human CTLA recepto
40	81	7.5	187	20	W97615	Human CTLA recepto
41	81	7.5	187	20	W97610	Human CTLA4 recept
42	81	7.5	211	20	W87560	Human CTLA4 recept
43	81	7.5	212	15	R31040	Human CTLA4 recept
44	81	7.5	212	15	R60134	CTLA4 receptor fus
45	81	7.5	212	16	R77642	Full length CTLA4

#### ALIGNMENTS

RESULT	1
ID	W75956 standard; Protein: 199 AA.
W75956	
XX	W75956;
XX	11-DEC-1998 (first entry)
XX	Human cell surface protein #1.
XX	Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
XX	signal transduction; autoimmune disorder; allergy; diagnosis;
XX	mitogen-stimulated.
OS	Homo sapiens.
XX	W09838216-A1.
PN	03-SEP-1998.
XX	27-FEB-1998; 98WO-JP00837.
XX	26-FEB-1998; 98JP-0062217.
PR	27-FEB-1997; 97JP-0062290.
XX	(NLSB ) JAPAN TOBACCO INC.
XX	Tamabani T, Tezuka K;
XX	WPT: 1998-481144/41.
DR	N-PSDB: V53198.
XX	Cell surface molecule expressed in thymocytes and lymphocytes and -
PT	mediating signal transduction and cell adhesion, and antibodies to

PT It useful in treatment of auto:immune and allergic disorders.  
 XX  
 PS Claim 2; Page 99-101; 149pp; Japanese.  
 XX  
 CC The present sequence represents a human cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognizing the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains  
 CC the amino acid sequence FDPDPF in its extracellular region and the  
 CC sequence YNMF in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of autoimmune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.  
 XX  
 SO Sequence 199 AA;

Query Match 99.0%; Score 1067.5; DB 19; Length 199;  
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;  
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MRSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGVQILCKYPIVQGFKKMLKGGQ 60  
 DB 1 mksglwyffflcrlirkvltgeingsanyemfifhngvqilckypdivqgfkmgllkggq 60  
 QY 61 ILCDLRTKSGMNTVSIKSLKFCQSLSNNSVSEFLYNLDHSHANYFCNLSTFDPDPFK 120  
 DB 61 ilcdlrtksgmntvsikslkfcqslnnsvsfellynldshanyfcnlstfdppfk 120  
 QY 121 VTLTGLIHLHYESQLCCQLKFWLPIGCAAF-VYCILGLCILCHLTTRKKYSSSVHDPNGEY 179  
 DB 121 vtltgylhlhyesqlccqlkfwlpigcaafvvcilgclilcwltkkkysssvhdpngey 180  
 QY 180 MFMRAVNTAKKSRLTDVTL 198  
 DB 181 mfmravntakksrltdvtl 199

RESULT 2  
 W75957  
 ID W75957 standard; Protein; 199 AA.  
 XX  
 AC W75957;  
 XX  
 DT 11-DEC-1998 (first entry)  
 XX  
 DE Human cell surface protein #2.  
 XX  
 KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;  
 KW signal transmission; autoimmune disorder; allergy; diagnosis;  
 KW mitogen-stimulated.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9838216-A1.  
 XX  
 PD 03-SEP-1998.  
 XX  
 PF 27-FEB-1998; 98WO-JP00837.  
 XX  
 PR 26-FEB-1998; 98JP-0062217.  
 PR 27-FEB-1997; 97JP-0062290.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 XX  
 PI Tamatani T, Tezuka K;  
 XX  
 DR WPI; 1998-481144/A1.  
 DR N-PSDB; V53199.  
 XX  
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -  
 PT mediating signal transmission and cell adhesion, and antibodies to

PT It useful in treatment of auto:immune and allergic disorders.  
 XX  
 PS Claim 9; Page 101-105; 149pp; Japanese.  
 XX  
 CC The present sequence represents a human cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognizing the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains  
 CC the amino acid sequence FDPDPF in its extracellular region and the  
 CC sequence YNMF in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of autoimmune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.  
 XX  
 SO Sequence 199 AA;

Query Match 99.0%; Score 1067.5; DB 19; Length 199;  
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;  
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MRSGLWYFFFLCRLIKVLTGEINGSANYEMFIFHNGVQILCKYPIVQGFKKMLKGGQ 60  
 DB 1 mksglwyffflcrlirkvltgeingsanyemfifhngvqilckypdivqgfkmgllkggq 60  
 QY 61 ILCDLRTKSGMNTVSIKSLKFCQSLSNNSVSEFLYNLDHSHANYFCNLSTFDPDPFK 120  
 DB 61 ilcdlrtksgmntvsikslkfcqslnnsvsfellynldshanyfcnlstfdppfk 120  
 QY 121 VTLTGLIHLHYESQLCCQLKFWLPIGCAAF-VYCILGLCILCHLTTRKKYSSSVHDPNGEY 179  
 DB 121 vtltgylhlhyesqlccqlkfwlpigcaafvvcilgclilcwltkkkysssvhdpngey 180  
 QY 180 MFMRAVNTAKKSRLTDVTL 198  
 DB 181 mfmravntakksrltdvtl 199

RESULT 3  
 Y08026  
 ID Y08026 standard; Protein; 199 AA.  
 XX  
 AC Y08026;  
 XX  
 DT 08-JUL-1999 (first entry)  
 XX  
 DE Human activated T-lymphocyte protein 8F4.  
 XX  
 KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;  
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;  
 KW T cell activation; cytokine synthesis; regulatory element; B cell;  
 KW T cell-dependent antibody production; treatment; prevention; cancer;  
 KW autoimmune disease; transplant rejection; immune system regulation;  
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9915553-A2.  
 XX  
 PD 01-APR-1999.  
 XX  
 PF 23-SEP-1998; 98WO-DE02896.  
 XX  
 PR 11-MAY-1998; 98DE-1021060.  
 PR 23-SEP-1997; 97DE-1041929.  
 XX  
 PA (DEKO-) DEUT KOCH INST ROBERT.  
 PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.  
 XX  
 PI Kroczeck R;  
 XX  
 DR WPI; 1999-276975/23.

DR N-PSDB: X37661.  
 XX Polypeptide 8F4 co-stimulates T cells and is present only on  
 PT activated cells  
 XX  
 PS Claim 2; Page 24; 47pp; German.  
 XX  
 CC This invention describes a novel human protein, 8F4, and its encoding  
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+  
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,  
 CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,  
 CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a  
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies  
 CC proliferation of T cells, synthesis of certain cytokines and other  
 CC regulatory agents, and improves T cell-dependent antibody production  
 CC by B cells. Agents that inhibit 8F4 are used to treat or prevent  
 CC autoimmune diseases, to prevent transplant rejection and to treat  
 CC disorders of immune system regulation. 8F4, or cells that express it,  
 CC is/are used to treat or prevent cancers, acquired immune deficiency  
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).  
 XX  
 SQ Sequence 199 AA:

Query Match 99.0%; Score 1067.5; DB 20; Length 199;  
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;  
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MKSGLYEFLFCRLRIKVLGEINGSANYEMFTHNGVQIICKYDPIVOQFMQLKGGQ 60  
 DB 1 mksqlywfflfcrlrikvltgelingsanyemfthngvqllckypdvqfkmqlkqg 60  
 OY 61 ILCDLTTRKGSNTVSIKSKCHSOLSNNSVFFLYLDHSHANYFCNLSIDPPPFK 120  
 DB 61 ilcdlttrkgsntvsiiskchsqslsnsvsfflyldshshanyfcnlsidpppfk 120  
 OY 121 VTLTGYLHIYESQCCOLKEWLPICGAAF-VVCILGCLICWLTKRKYSSVHDPNGEY 179  
 DB 121 vltlgylyhiyesqccqlkfwlpigcaafvvcilgcllcwltkrkyssvhdnpngey 180  
 OY 180 MEMRAVNTAKKSRLLDTVTL 198  
 DB 181 mfmravntakkerltdvcl 199  
 OY 1 T 4  
 ID B08731 standard; Protein; 199 AA.  
 AC B08731:  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human CRP1 polypeptide.  
 XX  
 KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;  
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;  
 KW T cell proliferation; T-cell mediated disorder.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key  
 FT Peptide 1..20 location/qualifiers  
 FT /note- "signal peptide"  
 FT 21..199  
 FT /note- "mature protein"  
 FT 21..140  
 FT /note- "extracellular domain"  
 FT 141..161  
 FT /note- "predicted transmembrane domain"  
 FT 162..199  
 FT Domain  
 XX /note- "intracellular domain"  
 XX

PN W0200046240-A2.  
 XX  
 XX 10-AUG-2000.  
 PD  
 XX  
 PF 27-JAN-2000; 2000WO-US01871.  
 XX  
 PR 03-FEB-1999; 99US-0244448.  
 PR 08-MAR-1999; 99US-0264527.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Yoshinaga SK;  
 DR WPI: 2000-543476/49.  
 DR N-PSDB: A64558.  
 XX  
 PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful  
 PT in the treatment, prevention and diagnosis of T cell mediated disorders  
 PT  
 XX  
 PS Disclosure: Fig 13A; 174pp; English.  
 PS  
 CC The present sequence represents a CRP1 (CD28 related protein-1)  
 CC polypeptide. The specification also describes a B7RP1 (B7 related  
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte  
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are  
 CC predicted to be a type I transmembrane protein. The nucleic acids are  
 CC useful for regulating T cell activation or proliferation in an animal.  
 CC The polypeptides are useful for treating, preventing ameliorating or  
 CC diagnosing a T-cell mediated disorder in an animal. They can also be  
 CC used to identify test molecules that bind to the polypeptides.  
 XX  
 SQ Sequence 199 AA:

Query Match 99.0%; Score 1067.5; DB 21; Length 199;  
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;  
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MKSGLYEFLFCRLRIKVLGEINGSANYEMFTHNGVQIICKYDPIVOQFMQLKGGQ 60  
 DB 1 mksqlywfflfcrlrikvltgelingsanyemfthngvqllckypdvqfkmqlkqg 60  
 OY 61 ILCDLTTRKGSNTVSIKSKCHSOLSNNSVFFLYLDHSHANYFCNLSIDPPPFK 120  
 DB 61 ilcdlttrkgsntvsiiskchsqslsnsvsfflyldshshanyfcnlsidpppfk 120  
 OY 121 VTLTGYLHIYESQCCOLKEWLPICGAAF-VVCILGCLICWLTKRKYSSVHDPNGEY 179  
 DB 121 vltlgylyhiyesqccqlkfwlpigcaafvvcilgcllcwltkrkyssvhdnpngey 180  
 OY 180 MEMRAVNTAKKSRLLDTVTL 198  
 DB 181 mfmravntakkerltdvcl 199  
 DB  
 RESULT 5  
 ID Y92213 standard; Protein; 198 AA.  
 XX  
 AC Y92213:  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Human Th2-specific polypeptide, h1228.  
 XX  
 KW h1228: Th2-specific; T helper cell; anti-inflammatory; antiarthritic;  
 KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;  
 KW antiproliferative; antistimulatory; antiallergic; anti-viral; optalmatological;  
 KW CTRA-4; nephrotoxic; anti-HIV; antibacterial.  
 XX  
 OS Homo sapiens.  
 XX

Key	Location/Qualifiers
Peptide	113..118
Peptide	/label="conserved_ppp_motif /note="common in CD28 and CTLA-4"
Peptide	178..181
Peptide	/label="YXXM_motif /note="common in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity"
Peptide	WO200019968-A1.
Peptide	13-APR-2000.
Peptide	06-OCT-1999; 99WO-US23156.
Peptide	07-OCT-1998; 98US-0168229.
Peptide	26-FEB-1999; 99US-0258670.
Peptide	06-OCT-1999; 99US-0413136.
Peptide	(MILL-) MILLENNIUM PHARM INC.
Peptide	Jechar S, Manning S, Coyle AJ, Gutierrez-ramos J; WPI; 2000-303619/26.
Peptide	N-PSDB; A09056.
Peptide	T helper (Th) 2 nucleic acids and encoded proteins, useful for the diagnosis and treatment of immune and respiratory disorders such as Crohn's diseases, arthritis, insulin dependent diabetes and autoimmunity
Peptide	Claim 16; Page 138-139; 159Pp; English.
Peptide	This Th2-specific polypeptide, which has similarity to human CD28 and human CTLA-4 is encoded by human orthologue h1228.
Peptide	A novel method for modulating a Th2 response, an immune response, or suppressing airway inflammation or hyperresponsiveness in a mammal, comprises administering a Th2-specific polypeptide of the invention, an antibody to such a polypeptide or allelic variants of the genes. The novel DNA and polypeptide sequences are useful for treatment and diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases, arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis, dermatitis, psoriasis, graft rejection, graft versus host diseases, sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis, viral infections (including human immunodeficiency virus (HIV)), bacterial infections, bronchitis, cystic fibrosis, diphtheria, empyema, pneumonia, and Legionnaires disease.
Peptide	Sequence 198 AA:
Peptide	Sequence Match 97.6%; Score 1052; DB 21; Length 198;
Peptide	Best Local Similarity 99.0%; Pred. No. 4.9e-111;
Peptide	Matches 197; Conservative 0; Mismatches 0; Indels 2; Gaps 2
Peptide	1 M K S G L W F P F L F C L R I K V L T G E I N G S A N Y D M F F H N G C V O I L C K Y P D I V O O F K M O L I K G C O 60
Peptide	1 m k s g l w y f f l f c l r i k v l t g e i n g s a n y e m i f h n g v q l l c k y p d i v q f k m q l l k g q 60
Peptide	61 I I C D L T K T K G S N W Y S I K S L F C H S O L S N S V S P F L Y N D H S H A N Y F C N L S T I P P P R K 120
Peptide	61 I I C D L T K L K G S N V S I K S I K C H q a b s m s v f l y n d h s h a n y f c n l s i f d p p r k 120
Peptide	121 V T L G G Y L H I Y E S Q L C C Q L K F W L P T G C A F - V V C I L G C I L I C W L T K K K Y S S V H D P N G E Y 179
Peptide	121 v e l t g g y l h i y e s q l c c q k f w l p r i g c a a f v v c l l g c i l c w l t - k k y s s a v h d p n g e y 179
Peptide	180 M E M R A V N T A K K S R L D V T L 198
Peptide	180 m e m r a v n t a k k s r l d v t l 198

Query Match	Best Local Similarity	69.3%	Pred. No. 2.9e-74;	Length 200;
Matches 138;	Conservative 20;	Mismatches 39;	Indels 2;	Gaps 2

OY		1	MKSLWAEFFELCKIRKVLTEINGSANVEAFIPHNCGVOLLKPITYVOQFMOLLKG90	60
Dd		1	mkyfchvifrcflirlllygelingsadhmfsfhngsvqscckypetvqqlkmrlfrere	60
OY		61	ILCDLRTKSGNMTVSIKSLKFCHSOLSNNSVFPLYNDHSHANYFCNLISFPDPPEFK	120
Dd		61	vlccltktgsgnavsknpmlcyllyhnsmnsvfllnpsdsqsyfcsislfdppptq	120
OY		121	V-TITGTVLHIYESQLCCQLEKFLPIEGCAFAVCYL-GCILICWLTKRYSVDHPNGE	178
Dd		121	ernlsggyllhyesqccqllkwlpygcaafvvallfgcillilwtskkkgssvndpnse	180
OY		179	YMFMRAVNFTAKKSRLDYDT	197
Dd		181	yfmavaytnkksrflagvt	199
B	T	7		
ID	B08723		standard; Protein; 200 AA.	
XX	B08723;			
XX	02-JAN-2001	(first entry)		
DE	Amino acid sequence of a murine CRP1 polypeptide.			
KX	CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;			
KW	T-lymphocyte activation; type I transmembrane protein; T cell activation,			
KM	T cell proliferation; T-cell mediated disorder.			
XX	Mus sp.			
OS				
FH	Key	Location/Qualifiers		
FT	Peptide	1..20		
FT		/note= "signal peptide"		
FT	Protein	21..200		
FT		/note= "mature protein"		
FT	Domain	21..145		
FT		/note= "extracellular domain"		
FT	Domain	146..163		
FT		/note= "predicted transmembrane domain"		
FT	Domain	164..200		
FT		/note= "intracellular domain"		
XX	MO200046240-A2.			
PD	10-AUG-2000.			
XX				
PF	27-JAN-2000; 2000MO-USO1871.			
XX				
PR	03-FEB-1999; 99US-0244448.			
PR	08-MAR-1999; 99US-0264527.			
XX				
XA	(AMGE-) AMGEN INC.			
XX				
PI	yoshinaga SK;			
XX				
DR	WPI: 2000-543476/49.			
DR	N-PDSB; A64554.			
XX				
PT	Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful			
PT	in the treatment, prevention and diagnosis of T cell mediated disorders			
PS	-			
XX				
XX	Claim 11; Fig 1A; 17app; English.			
CC	The present sequence represents a CRP1 (CD28 related protein-1)			
CC	polypeptide. The specification also describes a B7RP1 (B7 related			
CC	protein-1) polypeptide. The polypeptides are involved in T-lymphocyte			
CC	activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are			
CC	predicted to be a type I transmembrane protein. The nucleic acids are			
CC	useful for regulating T cell activation or proliferation in an animal.			

[illegible]







PT Novel recombinant virus useful as immunomodulators, particularly in  
PT vaccines  
PS Disclosure; Fig 4A; 230pp; English.  
XX  
CC This sequence represents feline CD28, as deduced from isolated  
CC peripheral blood mononuclear cell cDNA (see 234839). Manipulating  
CC the expression of CD28 or CTLA-4 (and/or their co-stimulatory  
CC ligands CD80 and CD86) regulates T cell proliferation and cytokine  
CC release. The invention relates to a recombinant virus that contains  
CC at least one foreign nucleic acid, inserted into a nonessential  
CC genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4  
CC protein, or their immunogenic fragments, and is expressed when the  
CC recombinant virus is introduced into a suitable host. The invention  
CC also provides: a recombinant virus further comprising a foreign  
CC nucleic acid encoding an immunogen derived from a feline pathogen;  
CC recombinant viruses capable of enhancing an immune response to  
CC protect against disease; recombinant viruses expressing antisense  
CC sequences, capable of suppressing an immune response in a feline,  
CC e.g. for treatment of autoimmune disease or transplant rejection;  
CC and recombinant viruses expressing DNA encoding CD80 and/or CD86  
CC used to reduce or eliminate a tumour in cats.

Sequence 221 AA:  
Query Match 13.1%; Score 141; DB 21; Length 221;  
Best Local Similarity 28.1%; Pred. No. 6.3e-08;  
Matches 45; Conservative 22; Mismatches 63; Indels 30; Gaps 9;  
QY 32 IFHNGVQIICKRYPD--IVQOFKMQLLKGGQIICDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
Db 31 vvynevevnijsckylhfnfskfraslkygdasavevcvngnshqpgfysgfdcdgk 90  
QY 87 LSNNVSFFFLYNDHSHANYFCNLISFDPPPF--KVTLTGGLHYIESQLC-CQLK--- 140  
Db 91 lgnctvfyrlnlfngtdlyfckievmypppyldneksngtlhvxekhlcpaqlspes 150  
QY 141 ---FWLPICGAAPVC--ILG-----CILICMLTKKK 167  
Db 151 skptfw-----alvvvggllgfyglatvalgacwmktr 184

RESULT 13  
Y32279 standard; Protein: 221 AA.  
XX  
AC Y32279;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
IT Cat CD28 receptor.  
XX  
CD28; receptor; cat; vaccine; feline immunodeficiency virus;  
KM FIV; feline leukaemia virus; feline infectious peritonitis virus;  
KM feline panleukopenia virus; feline calicivirus; feline reovirus-3;  
KM feline rotavirus; feline coronavirus; feline syncytial virus;  
KM feline sarcoma virus; feline herpesvirus; feline Borna disease;  
KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;  
KM parasite; autoimmune disease; transplant rejection; therapy.  
XX  
OS Felis domesticus.  
XX  
PN MO9957271-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 30-APR-1999; 99MO-0509502.  
XX  
PR 01-MAY-1998; 98US-0071699.  
XX  
PA (TEXA ) TEXAS A & M SYSTEM.  
XX

PI Collison EW, Hash SM, Choi I;  
XX WPI: 2000-052972/04.  
DR N-PDB; 234786.  
XX  
PT Novel feline proteins used to produce feline vaccines which prevent  
PT infectious disease or to promote growth in homologous or heterologous  
PT species -  
PS Example 1A; Fig 4A; 186pp; English.  
XX  
CC The present sequence represents feline CD28 receptor. The  
CC coexpression of CD28 with CD80 (see Y32276) or CD86 (see Y32278)  
CC and a tumour antigen or an antigen from a pathogenic organism has  
CC the ability to activate or enhance activation of T-lymphocytes,  
CC inducing the production of cytokines. The invention provides  
CC isolated nucleic acids encoding feline CD86 (B7-2) ligand, feline  
CC CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4  
CC (CD152) receptor, as well as vectors comprising the nucleic acids,  
CC and polypeptides encoded by the nucleic acids. It also provides  
CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and  
CC further comprising immunogens derived from pathogens, especially  
CC feline immunodeficiency virus (FIV), feline leukaemia virus,  
CC feline infectious peritonitis virus, feline panleukopenia virus,  
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline  
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline  
CC herpesvirus, feline Borna disease virus, rabies virus, chlamydia,  
CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial  
CC pathogen, or parasite (all claimed). Vaccines capable of  
CC enhancing an immune response, and vaccines capable of suppressing  
CC an immune response (suitable for treating an autoimmune disease  
CC or tissue or organ transplant rejection) are claimed.

Sequence 221 AA:  
Query Match 13.1%; Score 141; DB 21; Length 221;  
Best Local Similarity 28.1%; Pred. No. 6.3e-08;  
Matches 45; Conservative 22; Mismatches 63; Indels 30; Gaps 9;  
QY 32 IFHNGVQIICKRYPD--IVQOFKMQLLKGGQIICDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
Db 31 vvynevevnijsckylhfnfskfraslkygdasavevcvngnshqpgfysgfdcdgk 90  
QY 87 LSNNVSFFFLYNDHSHANYFCNLISFDPPPF--KVTLTGGLHYIESQLC-CQLK--- 140  
Db 91 lgnctvfyrlnlfngtdlyfckievmypppyldneksngtlhvxekhlcpaqlspes 150  
QY 141 ---FWLPICGAAPVC--ILG-----CILICMLTKKK 167  
Db 151 skptfw-----alvvvggllgfyglatvalgacwmktr 184

RESULT 14  
R20805  
ID R20805 standard; Protein: 220 AA.  
XX  
AC R20805;  
XX  
DT 21-MAY-1992 (first entry)  
XX  
DE Human CD28 antigen.  
XX  
KM cloning technique; cell surface antigen; immunodiagnosis;  
KM tumour.  
XX  
OS Homo sapiens.  
XX  
OS  
FH Key 1.18 Location/Qualifiers  
FT Peptide 1..18  
FT Protein 19..220 /label= signal  
FT Modified-site 37..39

FT		/label- N-linked_glycosylation
FT	Modified-site	71..73
FT	Modified-site	/label- N-linked_glycosylation
FT	Modified-site	92..94
FT	Modified-site	/label- N-linked_glycosylation
FT	Modified-site	105..107
FT	Modified-site	/label- N-linked_glycosylation
FT	Modified-site	129..131
FT	Region	/label- N-linked_glycosylation
XX		153..179
XX		/label- transmembrane
PN	W09201049-A.	
PD	23-JAN-1992.	
XX		
P	15-JUL-1990;	90WO-US04986.
P	13-JUL-1990;	90US-0553759.
PA	(GEHO-) GEN HOSPITAL CORP.	
XX		
PI	Seed B, Aruffo A, Amlot M;	
DR	WPI; 1992-056864/07.	
DR	N-PSDB; Q21167.	
XX		
PT	New CD53 cell surface antigen and DNA encoding it - for	
PT	immuno-therapy and diagnosis of haematopoietic neoplasms, etc.	
PS		
PS	Example 3; Fig 7; 160pp; English.	
XX		
CC	The CD28 antigen amino acid sequence was predicted from the	
CC	nucleotide sequence of a cDNA clone isolated from a human	
CC	lymphoblastoid cell line YJ library using the antibody enrichment	
CC	method (see Q21167). The sequence of the CD28 antigen has	
CC	substantial homology with mouse and rabbit immunoglobulin	
CC	heavy chain variable regions over a domain spanning almost the	
CC	entire extracellular portion of CD28.	
XX		
S0	Sequence 220 AA;	
Query Match 12.6%; Score 136; DB 13; Length 220;		
Fast Local Similarity 24.6%, Pred. No. 2.3e-07;		
Matches 42; Conservative 31; Mismatches 76; Indels 22; Gaps		
OY	30 MEIFNNGQGIQLCKPPD--IVQFKMQLKGGQIICDLCTRTKGSGN---TVSIRKSIFCH 84	
Dd	28 mlvaydnawnlsckysynlfrefraashkglidsavevcvygynsqqlqyysktgfncd 87	
OY	85 SOLSNNSVSFELYLNIDHSHANYFCNLSTIEDPPF--KVTLTGGLHYESOLC----- 136	
Dd	88 gllgneavstfygnilynvqtdiyfcklewmypppyldneksngtlthvkgkhlcpslfp 147	
OY	137 -CQLEFWLPICGAARVC---ILCIIICLWLTKKKYSVVDPRNGEYFM 182	
Dd	148 gpskfivwlvvvvgviacysallvtcvaflfwyrskr-srlhn---sdynnmm 194	
RESULT 15		
R27103		
ID R27103	standard; Protein; 220 AA.	
AC R27103:		
XX		
DT 25-FEB-1993	(first entry)	
XX		
DE Sequence encoded by the CD28 gene.		
XX		
KW CD28 protein; T-cell immune response; Tp44; differentiation antigen;		
XX membrane protein.		

[illegible]

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:03 ; Search time 14.16 Seconds

(without alignments)  
960.956 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078  
Sequence: 1 MMSGIMYFFLFCLIRKIVLTG.....YMFRAVNTAKSRLLDVL 198

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.67:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067.5	99.0	199	2 S78540	Inducible T-cell c
2	695.5	64.5	200	2 JC7397	activation-inducib
3	690.5	64.1	216	2 JC7396	T-cell surface gly
4	157.5	14.6	218	2 S24413	CD28 precursor - r
5	147	13.6	221	2 I46689	T-cell surface gly
6	141.5	13.1	218	2 A43523	cell surface gly
7	138	12.8	173	2 I46157	T-cell surface gly
8	136	12.6	220	1 RMH028	cell surface gly
9	105.5	9.8	221	2 S25168	CH28 protein - ch
10	93	8.6	223	2 A29063	hypothetical prote
11	86	8.0	223	2 T18986	cytotoxic T-lympho
12	86	8.0	383	2 T21946	hypothetical prote
13	86	8.0	635	2 JC5896	killer cell inhibi
14	85.5	7.9	223	2 T09536	cytotoxic T-lympho
15	83.5	7.7	285	2 D69440	conserved hypotet
16	83	7.7	186	2 S08614	cytotoxic T-lympho
17	82.5	7.7	248	1 COBEAL	probable glycoprot
18	81.5	7.6	330	2 A40071	Fc gamma (IlgG) rec
19	81.5	7.6	330	2 I49660	Fc gamma-1/gamma-2
20	81.5	7.6	363	2 T32479	hypothetical prote
21	81.5	7.6	1584	2 S57161	hypothetical prote
22	81	7.5	276	2 S20690	31.6k hypothetical
23	81	7.5	302	1 WMBE1E	secretory compleme
24	81	7.5	360	1 WMBE2E	membrane bound com
25	79.5	7.4	283	1 FCMSC1	Fc gamma (IlgG) rec
26	79.5	7.4	680	2 JC5895	killer cell inhibi
27	78.5	7.3	231	2 T23136	hypothetical prote
28	78	7.2	235	2 I50610	T-cell surface gly
29	77.5	7.2	220	2 A48581	37k proline-rich s

30	77.5	7.2	546	2 S52053	cytochrome-c oxida
31	77	7.1	1070	2 JC4593	protein-tyrosine k
32	76	7.1	301	2 I54209	hypothetical prote
33	76	7.1	323	2 S06946	Fc gamma (IlgG) rec
34	75.5	7.0	261	2 S29360	Fc gamma (IlgG) rec
35	75.5	7.0	277	2 T21330	hypothetical prote
36	75.5	7.0	1132	1 OSBP1	host specificity p
37	75.5	7.0	2135	2 T14602	variant-specific s
38	74.5	6.9	763	2 S17998	gene COX1 intron 4
39	74	6.9	223	2 I46696	CTLA-4 precursor -
40	74	6.9	258	2 E71646	hypothetical prote
41	74	6.9	496	2 JH0165	glycine receptor b
42	74	6.9	496	2 S46459	glycine receptor b
43	74	6.9	497	2 G02031	glycine receptor b
44	73.5	6.8	275	2 S61179	probable membrane
45	73.5	6.8	322	2 I48207	corticotropin-rele

#### ALIGNMENTS

```
RESULT 1
S78540
Inducible T-cell co-stimulator ICOS precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999
C:Accession: S78540; S78748; S78749
R:Kroczeck, R.
Submitted to the Protein Sequence Database, June 1998
A:Reference number: S78540
A:Accession: S78540
A:Molecule type: mRNA
A:Residues: 1-199 <KRO>
A:Experimental source: cell line MOLT-4V
R:Hutloff, A.; Dittlich, A.M.; Beier, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop
Nature 397, 263-266, 1999
A:Title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela
A:Reference number: S78748; MUID:99127892
A:Accession: S78748
A:Molecule type: mRNA
A:Residues: 1-199 <HUT1>
A:Experimental source: cell line MOLT-4V
A:Accession: S78749
A:Molecule type: Protein
A:Residues: 'X', 193-198 <HUT2>
A:Experimental source: cell line MOLT-4V
C:Complex: homodimer
C:Superfamily: immunoglobulin homology
F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>
F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT>
F:21-138/Domain: extracellular #status predicted <EXT>
F:26-132/Domain: immunoglobulin homology <IMM>
F:139-164/Domain: transmembrane #status predicted <TMN>
F:165-199/Domain: intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.0%; Score 1067.5; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 MMSGIMYFFLFCLIRKIVLTGELTNGSANYEMFPHNGVQILCKYPDIVQGRKMLLKGGQ 60  
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Db 1 MMSGIMYFFLFCLIRKIVLTGELTNGSANYEMFPHNGVQILCKYPDIVQGRKMLLKGGQ 60  
|||||  
Qy 61 ILCDLTTRKSGSNVYSISLKFCHSOLSNNSVSFFLYMLDISHSHANYRCNLSIDPPPFK 120  
|||||  
Db 61 ILCDLTTRKSGSNVYSISLKFCHSOLSNNSVSFFLYMLDISHSHANYRCNLSIDPPPFK 120  
|||||  
Qy 121 VTLNGGYLHIESQLCCOLKFWLPICGAAV-VCCILGICILCWLTKRKYSSVHDPNGEY 179  
|||||  
Db 121 VTLNGGYLHIESQLCCOLKFWLPICGAAV-VCCILGICILCWLTKRKYSSVHDPNGEY 180  
|||||



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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:03 ; Search time 13.01 Seconds  
(without alignments)  
292.371 Million cell updates/sec

Title: US-09-509-283-2  
Perfect score: 1078  
Sequence: 1 MRSGLWTFPLFLCLRIKIVLTG.....YMFRAVNTAKKSLIDVTL 198

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Seatched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159.5	14.8	218	3	US-08-228-208A-20
2	143	13.3	225	1	US-08-505-058-4
3	143	13.3	225	2	US-08-459-818-24
4	143	13.3	225	2	US-08-889-666-24
5	143	13.3	225	2	US-08-465-078-24
6	143	13.3	225	2	US-08-725-776-24
7	143	13.3	225	2	US-08-488-062-24
8	135.5	12.6	218	3	US-08-228-208A-19
9	130	12.1	220	1	US-08-228-208A-21
10	129.5	12.0	225	1	US-08-505-058-3
11	128.5	12.0	225	2	US-08-459-818-23
12	128.5	12.0	225	2	US-08-889-666-23
13	128.5	12.0	225	2	US-08-465-078-23
14	129.5	12.0	225	2	US-08-725-776-23
15	129.5	12.0	225	2	US-08-488-062-23
16	121.5	11.3	223	1	US-08-505-058-5
17	121.5	11.3	223	2	US-08-459-818-25
18	121.5	11.3	223	2	US-08-889-666-25
19	121.5	11.3	223	2	US-08-465-078-25
20	121.5	11.3	223	2	US-08-725-776-25
21	121.5	11.3	223	2	US-08-488-062-25
22	120.5	11.2	367	3	US-08-630-172-19
23	119.5	11.1	134	3	US-08-630-172-3
24	97.5	9.0	221	3	US-08-228-208A-22
25	89.5	8.3	117	3	US-08-529-878B-39
26	84.5	7.8	226	1	US-08-505-058-6
27	84.5	7.8	226	2	US-08-459-818-26

28	84.5	7.8	226	2	US-08-889-666-26	Sequence 26, Appl
29	84.5	7.8	226	2	US-08-465-078-26	Sequence 26, Appl
30	84.5	7.8	226	2	US-08-725-776-26	Sequence 26, Appl
31	84.5	7.8	226	2	US-08-488-062-26	Sequence 26, Appl
32	83.5	7.7	223	3	US-08-228-208A-17	Sequence 17, Appl
33	81.5	7.6	330	2	US-08-332-562A-81	Sequence 81, Appl
34	81.5	7.6	330	2	US-08-332-562A-134	Sequence 134, App
35	81	7.5	187	1	US-08-067-684-14	Sequence 14, Appl
36	81	7.5	187	1	US-08-008-898-14	Sequence 14, Appl
37	81	7.5	187	2	US-08-459-818-14	Sequence 14, Appl
38	81	7.5	187	2	US-08-889-666-14	Sequence 14, Appl
39	81	7.5	187	2	US-08-465-078-14	Sequence 14, Appl
40	81	7.5	187	2	US-08-725-776-14	Sequence 14, Appl
41	81	7.5	187	2	US-08-488-062-14	Sequence 14, Appl
42	81	7.5	187	3	US-08-228-208A-14	Sequence 14, Appl
43	81	7.5	187	3	PCT-US95-06726-36	Sequence 36, Appl
44	80.5	7.5	234	1	US-08-505-058-1	Sequence 1, Appl
45	80.5	7.5	234	2	US-08-459-818-21	Sequence 21, Appl

#### ALIGNMENTS

RESULT 1  
US-08-228-208A-20  
Sequence 20, Application US/08228208A  
Patent No. 6090914  
GENERAL INFORMATION:  
APPLICANT: Linsley, Peter S.  
APPLICANT: Iedebetter, Jeffrey A.  
APPLICANT: Damle, Milin K.  
APPLICANT: Brady, William  
APPLICANT: Wallace, Philip M.  
TITLE OF INVENTION: CTLA4/CD2819 HYBRID FUSION  
TITLE OF INVENTION: PROTEINS AND USES THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 11150 Santa Monica Boulevard, Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/228, 208A  
FILING DATE: 15-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008, 898  
FILING DATE: 22-JAN-1993  
APPLICATION NUMBER: 07/723, 617  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B  
REGISTRATION NUMBER: 34, 470  
REFERENCE/DOCKET NUMBER: 30436-30US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310 445-1140  
TELEFAX: 310 445-9031  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-228-208A-20

	Query Match	14.8%	Score 159.5;	DB 3;	Length 218;
	Best Local Similarity	25.8%	Pred. No. 5.4e-117		
	Matches 40; Conservative	30;	Mismatches 66; Indels 19; Gaps 7.		
OY	30 MEFINGGVQILCKYPD--IVQQFMQLLKGQIICDLTKRTGSGNTVSINKSLK-----F 82	:	:	:	:
Dd	29 LLVYNNEEVLISCRSYNLAKERFASLYLK--VASDVECVCGNGNFYYQPQPRFNVGFN 86	:	:	:	:
OY	83 CHSGLSNNSVSFFFLYNLDHSHANYIFCULSTDPDF--KVTLTGAYLIYSOLC---- 136	:	:	:	:
Dd	87 CDGNEDNETHVFRLNNLLDVNNHTDIYFCKEIEVMYPPEYLDENEKSNGTHIIHKELCHQAOT 146	:	:	:	:
OY	137 QQLKFMLPIGCAPVVC--IIGCILIC--WLKKR 167	:	:	:	:
Dd	147 SPKLFWPLVVAVAGVLLCYGLLTVTLCITWNSRR 181	:	:	:	:

RESULT 2  
 US-08-505-058-4  
 Sequence 4, Application US/08505058  
 Invent No. 5773253  
 GENERAL INFORMATION:  
 APPLICANT: Linsley, Peter S.  
 APPLICANT: Ledbetter, Jeffrey A.  
 APPLICANT: Peach, Robert  
 TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 11150 Santa Monica Blvd., Suite 400  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/505,058  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/228,208  
 FILING DATE: 15-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Adriano, Sarah B.  
 REGISTRATION NUMBER: 34,470  
 REFERENCE/DOCKET NUMBER: 30436.30US11  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310-445-1140  
 TELEFAX: 310-445-9031  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 225 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-505-058-4

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Query Match      13.3%  Score 143;  DB 1;  Length 225;
Best Local Similarity 25.6%  Pred. No. 5e-09;
Matches 41;  Conservative 30;  Mismatches 65;  Indels 24;  Gaps 9

QY  30  MFIHNGVQIL-CRYP--IVQQRKMLKGGQILDLTKT-KSGNGTVSTKSLK---- 81
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db   30  LLYVDNNVSVLSKCYRYSNLAKERASLYKK--VNSDVGEVCGVNGNTYQPPFPNNG 87
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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[illegible]

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3
US-08-459-818-24
: Sequence 24, Application US/08459818
: Patent No. 5851795
:
: GENERAL INFORMATION:
:   APPLICANT: Linsley, Peter S.
:   APPLICANT: Ledbetter, Jeffrey A.
:   APPLICANT: Dame, Nltin K.
:   APPLICANT: Brady, William
:   TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
:   NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Merchant & Gould
:   STREET: 11150 Santa Monica Blvd., Suite 400
:   CITY: Los Angeles
:   STATE: California
:   COUNTRY: USA
:   ZIP: 90025
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Fastseq 2.0
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/459,818
:     FILING DATE: 02-JUN-1995
:     CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: Adriano, Sarah B.
:   REGISTRATION NUMBER: 34,470
:   REFERENCE/DOCKET NUMBER: 30436.3JUS02
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 310-445-1140
:     TELEFAX: 310-445-9031
:
: INFORMATION FOR SEQ ID NO: 24:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 225 amino acids
:     TYPE: amino acid
:     STRANDEDNESS:
:     TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-459-818-24

```

Query Match	13.3%	Score 143;	DB 2;	length 225;
Best Local Similarity	25.6%	Pred. No. 5e-09;		
Matches	41;	Conservative	30;	Mismatches 65; Indels 24; Gaps 9.
OY	30	MEIFHNGVQQLL-CRYPD--IVQDFKMLDLKGQGLLCLDTKK-KSGNTVSIKSLK----	81	
	:::::	:::::	:::::	:::::
Db	30	LLVYDNNVEXSLCSRYSNLLAKERASLYKG--VNSDYKVCVGNNGNTYQPPRPNNVG	87	
OY	82	-FCHSQSLNNSVSFFLYLLDHSHANYTCNLSIEDPPP--KVTLLTGYGLHYESQLC--	136	
	:::	:::	:::	:::
Db	88	FNCGDNFNEIVTFRLMLDNDHVEDIYFCKIEVMVPPRYLDNENKSGNTLIHKEKHLCHA	147	
OY	137	-----CQLKEWLPICGAFVVC--ILGILCLL--LTLTKK	167	
	:::	:::	:::	:::
Db	148	XXXOTSKEMLPVVAVAGVLGLLYVLTCLITNSR	187	

RESULT 4  
US-08-889-666-24  
; Sequence 24, Application US/08889666



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:23 ; Search time 22.68 Seconds

(without alignments)  
1023.244 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078  
Sequence: 1 MMSGLMWFFLFCLRIKVLG.....YMEKAVNTAKSRIDVTL 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.15:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mbc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067.5	99.0	199	4	Q9Y6W8
2	727	67.4	200	11	Q9WVS0
3	723.5	67.1	200	11	Q9JL17
4	695.5	64.5	200	11	Q9R1T7
5	690.5	64.1	216	11	Q9WVR9
6	142	13.2	221	11	Q9JLV4
7	141	13.1	221	6	Q9JLV4
8	141	13.1	221	6	Q9N214
9	139	12.9	221	6	Q9N0N8
10	138.5	12.8	219	6	Q9Y630
11	138	12.8	173	6	Q9Y630
12	93	8.6	988	5	Q28289
13	86	8.0	485	5	Q20139
14	86	8.0	635	11	Q55002
15	86	8.0	663	11	Q70434
16	84	7.8	223	11	Q9QZ27
17	84	7.8	419	13	Q9IA51
18	83.5	7.7	285	1	Q28747
19	83	7.7	209	4	Q9NYK4

20	83	7.7	223	11	Q9JLV3	Q9JLV3 marmota mon
21	82	7.6	296	14	Q73315	Q73315 human immun
22	81.5	7.6	223	11	Q62859	Q62859 ratulus norv
23	81.5	7.6	563	5	Q17395	Q17395 caenorhabdi
24	81	7.5	276	14	Q98822	Q98822 human adeno
25	81	7.5	276	14	Q64861	Q64861 human adeno
26	80.5	7.5	321	4	Q9UGF6	Q9UGF6 homo sapien
27	80	7.4	761	11	Q9Y630	Q9Y630 mus musculu
28	79.5	7.4	680	11	Q55001	Q55001 mus musculu
29	78.5	7.3	231	5	Q45668	Q45668 caenorhabdi
30	78.5	7.3	539	14	P88842	P88842 avian infec
31	78	7.2	235	13	Q90770	Q90770 gallus gall
32	78	7.2	269	4	Q95297	Q95297 homo sapien
33	77.5	7.2	546	8	Q35989	Q35989 trypanos
34	77	7.1	415	10	Q9LW05	Q9LW05 arabidopsi
35	76.5	7.1	539	14	P88839	P88839 avian infec
36	76.5	7.1	539	14	P88840	P88840 avian infec
37	76.5	7.1	539	14	P88843	P88843 avian infec
38	76.5	7.1	619	10	Q9XG51	Q9XG51 sorghum bic
39	76.5	7.1	863	10	Q9M0D8	Q9M0D8 arabidopsi
40	76	7.1	174	11	Q9Z1A7	Q9Z1A7 ratulus norv
41	76	7.1	192	14	Q11432	Q11432 avian adeno
42	76	7.1	448	11	Q88597	Q88597 mus musculu
43	76	7.1	450	4	Q75595	Q75595 homo sapien
44	76	7.1	450	4	Q9UN48	Q9UN48 homo sapien
45	76	7.1	948	5	Q9YDQ7	Q9YDQ7 drosophila

## ALIGNMENTS

RESULT 1  
ID Q9Y6W8 PRELIMINARY; PRT; 199 AA.  
AC Q9Y6W8;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DF 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM  
DE PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP TISSUE=BLOOD;  
RA Tezuka K., Tamatani T.;  
RT "Cell surface molecule mediating cell adhesion and signal  
transmission";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB021315; BAA82129.1; -;  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 199 AA; 22624 MW; 21AEC741C9BDC9FC CRC64;

Query Match 99.0%; Score 1067.5; DB 4; Length 199;  
Best Local Similarity 99.5%; Pred. No. 7.6e-106;  
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MMSGLMWFFLFCLRIKVLGGEINGSANYEMFPHNGGVQILKYPDIYQFMOLLKGGQ 60  
DB 1 MMSGLMWFFLFCLRIKVLGGEINGSANYEMFPHNGGVQILKYPDIYQFMOLLKGGQ 60  
QY 61 IICDLTKTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNIDHSNANYFCNLSIFPPPPK 120  
DB 61 IICDLTKTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNIDHSNANYFCNLSIFPPPPK 120  
QY 121 VLTGTGLHYISQQLCKLFWLPICGAAF-VVCIIGCTILCWLTKRKYSSVHPNGEY 179  
DB 121 VLTGTGLHYISQQLCKLFWLPICGAAFVVVCIIGCTILCWLTKRKYSSVHPNGEY 180

QY 180 MEMRAVNTAKSRLTDT 198  
 DB 181 MEMRAVNTAKSRLTDT 199

## RESULT 2

Q9WV50 PRELIMINARY; PRT; 200 AA.  
 AC Q9WV50; (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIN  
 DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).  
 GN CCIP OR ICOS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Tezuka K., Tamatani T.;  
 RL "Cell surface molecule mediating cell adhesion and signal  
 transmission.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=SPLEEN;  
 RA Wu D., Giamoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,  
 RA Matlis L.A., Rother R.P.;  
 RL "CCIP, A novel molecule that regulates T cell activation.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=SPLEEN;  
 RA Mages H.W., Hultlof A., Heuck C., Buchner K., Himmelbauer H.,  
 RA Oliveri F., Kroczeck R.A.;  
 RL "Molecular cloning and characterization of murine ICOS and  
 RT Identification of B7h as ICOS ligand.";  
 RL Eur. J. Immunol. 30:1040-1047 (2000).  
 DR EMBL; AB023132; BAA82126.1; -;  
 DR EMBL; AF257230; AAF70099.1; -;  
 DR EMBL; AJ250559; CAB71153.1; -;  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 200 AA; 22690 MW; 9B2278EACAB1D847 CRC64;

Query Match 67.4%; Score 727; DB 11; Length 200;  
 Best Local Similarity 69.3%; Pred. No. 1.3e-69;

Matches 138; Conservative 20; Mismatches 39; Indels 2; Gaps 2;

QY 1 MKSGLMFLEFLIKVLTGINSANTEMPIFHNGVQILCKPDYQOKMQLKGGQ 60  
 DB 1 MKPEYCHVFECFIRLTGINSADHRMFSFHNGVQISCKPEYVQOKMLFRFRE 60  
 QY 61 ILCDLTKSGNVTISIKSLKFCQSOLSNNSVFFLYNLDSHANYFCNLSTFDPPEFK 120  
 DB 61 VLCELTTKSGNAVSTIKNMLCLYHLSNNSVSFFLNPPDSQSYFCSLSTFDPPEFQ 120  
 QY 121 V-TLTGTYLHYESQLCCQLKFWLPICGAFFVCIL-GCILICMLTKKYSVHPDNGE 178  
 DB 121 ERNLGSGYTLHYESQLCCQLKFWLPVGCARFVVVLLFGCILITIMFSKKYGVHPDENSE 180  
 QY 179 YMFMAVNTAKSRLTDT 197  
 DB 181 YMFMAVNTAKSRLTDT 199

RESULT 3  
 Q9JUL17 PRELIMINARY; PRT; 200 AA.  
 IB Q9JUL17

AC Q9JUL17;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIN  
 DE PRECURSOR (CCIP PRECURSOR) (SURFACE PROTEIN).  
 GN CCIP OR ICOS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINAL INTRA-EPITHELIUM;  
 RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmento U., Guo J.,  
 RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Telford-Bladt A.,  
 RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,  
 RA Hul A., McCabe S.M., Scully S., Shalee C.L., Van G., Mak T.W.,  
 RA Senaldi G.;  
 RL "T-cell co-stimulation through B7RP-1 and ICOS.";  
 RL Nature 0:0-0 (2000).  
 DR EMBL; AF216748; AAF45150.1; -;  
 FT NON\_TER 200  
 SQ SEQUENCE 200 AA; 22709 MW; 87D97F0DC44ADCA7 CRC64;

Query Match 67.1%; Score 723.5; DB 11; Length 200;  
 Best Local Similarity 70.4%; Pred. No. 3.1e-69;

Matches 138; Conservative 19; Mismatches 34; Indels 5; Gaps 3;

QY 7 YF--FLFCURIKVLTGINSANTEMPIFHNGVQILCKPDYQOKMQLKGGQILC 63  
 DB 4 YFCRVFVFCFIRLTGINSADHRMFSFHNGVQISCKPEYVQOKMLFRFREYLC 63  
 QY 64 DLTKSGNVTISIKSLKFCQSOLSNNSVFFLYNLDSHANYFCNLSTFDPPEFKV-T 122  
 DB 64 ELTKSGNAVSTIKNMLCLYHLSNNSVSFFLNPPDSQSYFCSLSTFDPPEERN 123  
 QY 123 LTGTYLHYESQLCCQLKFWLPICGAFFVCIL-GCILICMLTKKYSVHPDNGEYMF 181  
 DB 124 LSGYTLHYESQLCCQLKFWLPVGCARFVVVLLFGCILITIMFSKKYGVHPDENSEYMF 183  
 QY 182 MRAVNTAKSRLTDT 197  
 DB 184 MAAVNTAKSRLTDT 199

## RESULT 4

Q9R1T7 PRELIMINARY; PRT; 200 AA.

AC Q9R1T7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIN  
 DE PRECURSOR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tezuka K., Tamatani T.;  
 RL "Cell surface molecule mediating cell adhesion and signal  
 transmission.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB023134; BAA82128.1; -;  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 200 AA; 22529 MW; 0A74C35581F129D4 CRC64;

Query Match 64.5%; Score 695.5; DB 11; Length 200;  
 Best Local Similarity 68.4%; Pred. No. 2.9e-66;  
 Matches 134; Conservative 17; Mismatches 40; Indels 5; Gaps 3;

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:48 ; Search time 9.54 Seconds  
(without alignments) 710.963 Million cell updates/sec

Title: US-09-509-283-2

Sequence: 1 MMSGLMYFFLFCLRIKIVLFG.....YMFMRVNTAKSKRLDVTL 198

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.5	14.4	218	1	CD28_RAT
2	147	13.6	221	1	P31042 rattus norv
3	141.5	13.1	218	1	P42069 oryctolagus
4	136	12.6	220	1	CD28_MOUSE
5	134.5	12.5	219	1	CD28_HUMAN
6	105.5	9.8	221	1	CD28_BOVIN
7	86	8.0	223	1	CD28_CHICK
8	85.5	7.9	223	1	CD28_MOUSE
9	82.5	7.7	223	1	CD28_HUMAN
10	81.5	7.6	330	1	CD28_MOUSE
11	81.5	7.6	330	1	CD28_MOUSE
12	81	7.5	1584	1	CD28_MOUSE
13	77.5	7.2	324	1	CD28_MOUSE
14	77	7.1	1070	1	CD28_MOUSE
15	76	7.1	448	1	CD28_MOUSE
16	76	7.1	448	1	CD28_MOUSE
17	76	7.1	448	1	CD28_MOUSE
18	75.5	7.0	261	1	CD28_MOUSE
19	75.5	7.0	261	1	CD28_MOUSE
20	75.5	7.0	261	1	CD28_MOUSE
21	74	6.9	1132	1	CD28_MOUSE
22	74	6.9	344	1	CD28_MOUSE
23	74	6.9	496	1	CD28_MOUSE
24	74	6.9	496	1	CD28_MOUSE
25	74	6.9	496	1	CD28_MOUSE
26	73.5	6.8	275	1	CD28_MOUSE
27	73.5	6.8	275	1	CD28_MOUSE
28	73.5	6.8	275	1	CD28_MOUSE
29	73.5	6.8	275	1	CD28_MOUSE
30	73	6.8	916	1	CD28_MOUSE
31	72	6.7	569	1	CD28_MOUSE
32	71.5	6.6	317	1	CD28_MOUSE
33	71.5	6.6	1154	1	CD28_MOUSE

34	71.5	6.6	1163	1	CD28_MOUSE
35	71.5	6.6	2768	1	CD28_MOUSE
36	71	6.6	329	1	CD28_MOUSE
37	71	6.6	372	1	CD28_MOUSE
38	71	6.6	524	1	CD28_MOUSE
39	71	6.6	634	1	CD28_MOUSE
40	71	6.6	1051	1	CD28_MOUSE
41	70.5	6.5	322	1	CD28_MOUSE
42	70.5	6.5	466	1	CD28_MOUSE
43	70.5	6.5	520	1	CD28_MOUSE
44	70.5	6.5	550	1	CD28_MOUSE
45	70.5	6.5	561	1	CD28_MOUSE

## ALIGNMENTS

RESULT 1	ID	CD28_RAT	STANDARD:	PRT:	218 AA.
AC	P31042:				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28 PRECURSOR.				
GN	CD28.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=DA; TISSUE=Lymphoid;				
RX	MEDLINE=92104640; PubMed=1309509;				
RA	Clark G.J., Dailman M.J.;				
RT	Identification of a cDNA encoding the rat CD28 homologue.;				
RL	Immunogenetics 35:54-57(1992).				
CC	- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1 AND B7-2 (B70).				
CC	- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND.				
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. STRONGEST SIMILARITY TO CTLA-4.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	EMBL, X55288; CAA39003.1; -				
DR	PIR, S38722; S38722.				
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.				
FT	SIGNAL	1	19		
FT	CHAIN	20	218		
FT	DOMAIN	20	150		
FT	TRANSMEM	151	177		
FT	DOMAIN	178	218		
FT	DOMAIN	29	138		
FT	CARBOHYD	72	72		
FT	CARBOHYD	93	93		
FT	CARBOHYD	106	106		
FT	CARBOHYD	130	130		
FT	SEQUENCE	218 AA;	25170 MW;		

Query Match 14.4%; Score 155.5; DB 1; Length 218;  
Best Local Similarity 25.8%; Pred. No. 3.1e-08;  
Matches 40; Conservative 29; Mismatches 67; Indels 19; Gaps 7;

QY 30 MFFHNGVQIICKYPD--IVQOFKMOILCDLTKGSGNTVSTKSLK-----F 82  
DB 29 LTVVDNNEVSLSCRSYSNLAKEFRASLYK--VNSDVEVCVGNNGFTQPOFRPNVGFN 86  
QY 83 CHSOLSNNSVSEFLYNLDHSHANYFCNLSEDPPEF--KVTLLGGLHYEQLC----- 136  
DB 87 CDGNEFNEVTFELMDVNDHTDYFCIEVMYPPPLDNEKSGTIIHKHHLCHAQT 146  
QY 137 COLKFWLPICGAAFYVC--ILGCLILC--WLTKRK 167  
DB 147 SPKLFMPLVVAGVLLCYGLLVTVLTICIIWTNRR 181  
RESULT 2  
CD28\_RABIT STANDARD; PRT; 221 AA.  
AC P42069;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28 PRECURSOR.  
GN CD28.  
OC Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID:9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B/J X CHB:HM;  
RX MEDLINE:95369849; PubMed:7642234;  
RA Isono T., Sato A.;  
RT "Cloning and sequencing of the rabbit gene encoding T-cell  
RT costimulatory molecules.";  
RT Immunogenetics 42:217-220(1995).  
CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1  
CC AND B7-2 (B70) (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. STRONGEST  
CC SIMILARITY TO CTLA-4.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: D49841; BAA08641.1; -  
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19 BY SIMILARITY.  
FT CHAIN 20 221 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN  
FT CD28.  
FT -----  
FT DOMAIN 20 150 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 151 177 POTENTIAL.  
FT DOMAIN 178 221 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 29 138 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 221 AA; 25307 MW; 3DF652C9CFC1AF13 CRC64;  
Query Match 13.6%; Score 147; DB 1; Length 221;  
Best Local Similarity 23.2%; Pred. No. 2.1e-07;  
Matches 39; Conservative 26; Mismatches 61; Indels 42; Gaps 7;  
QY 30 MFFHNGVQIICKYPD--IVQOFKMOILCDLTKGSGNTVSTKSLK-----F 82  
DB 29 LTVVDNNEVSLSCRSYSNLAKEFRASLYK--VNSDVEVCVGNNGFTQPOFRPNVGFN 86  
QY 83 CHSOLSNNSVSEFLYNLDHSHANYFCNLSEDPPEF--KVTLLGGLHYEQLC----- 136  
DB 87 CDGNEFNEVTFELMDVNDHTDYFCIEVMYPPPLDNEKSGTIIHKHHLCHAQT 146  
QY 137 COLKFWLPICGAAFYVC--ILGCLILC--WLTKRK 167  
DB 147 SPKLFMPLVVAGVLLCYGLLVTVLTICIIWTNRR 181

QY 81 KFCBSQLSNNSVSEFLYNLDHSHANYFCNLSEDPPEF--KVTLLGGLHYEQLC-- 136  
DB 87 -CDGKLGNETVTFELKLYVNGTDTDYFCIEVMYPPPLDNEKSGTIIHVEQHECPA 144  
QY 137 -----COLKFWLPICGAAFYVCILGCLIL-----CWLTTRK 167  
DB 145 HPSKSSSTLFW-----VLVVAGVLAFLYMLVTVALESCWMSKSK 184  
RESULT 3  
CD28\_MOUSE STANDARD; PRT; 218 AA.  
ID CD28\_MOUSE  
AC P31041;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28 PRECURSOR.  
GN CD28.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE:90217534; PubMed:2157764;  
RX Gross J.A., St John T., Allison J.P.;  
RT "The murine homologue of the T lymphocyte antigen CD28. Molecular  
RT cloning and cell surface expression.";  
RL J. Immunol. 144:3201-3210(1990).  
RN [2]  
RP SEQUENCE OF 156-218 FROM N.A.  
RX MEDLINE:91318145; PubMed:1713603;  
RA Harper K., Balzano C., Rouvier E., Matzel M.-G., Luciani M.F.,  
RA Golstein P.;  
RT "CTLA-4 and CD28 activated lymphocyte molecules are closely related  
RT in both mouse and human as to sequence, message expression, gene  
RT structure, and chromosomal location.";  
RL J. Immunol. 147:1037-1044(1991).  
CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1  
CC AND B7-2 (B70).  
CC -1- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. STRONGEST  
CC SIMILARITY TO CTLA-4.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: M34563; AAA37395.1; -  
DR EMBL: M74361; AAA37396.1; -  
DR PIR: A43523; A43523.  
DR MGI: 88327; Cd28.  
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19 BY SIMILARITY.  
FT CHAIN 20 218 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN  
FT CD28.  
FT -----  
FT DOMAIN 20 150 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 151 177 POTENTIAL.  
FT DOMAIN 178 218 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 29 138 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 187 189 VTT -> SDY (IN REF. 2).  
SQ SEQUENCE 218 AA; 25179 MW; A491439DD7EB8D7F CRC64;

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:04 ; Search time 19.85 Seconds

(without alignments)  
570.192 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198  
Sequence: 1 MKSGLMYFFFLCRLKIVLTG.....YMPRAVNPAKKSRIDVTL 198

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Sequences: 390729 seqs, 57163235 residues

Word size : 0

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A.Geneseq\_0401.\*  
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
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4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
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8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
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10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
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19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
21: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:\*  
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	76.8	198	21	Y92213 Human Th2-specific
2	152	76.8	199	19	W75956 Human cell surface
3	152	76.8	199	20	W75957 Human cell surface
4	152	76.8	199	20	Y08026 Human activated T-
5	152	76.8	199	21	B08731 Amino acid sequenc
6	152	76.8	200	19	W1874 Rat cell surface p
7	152	76.8	216	19	W1875 Rat cell surface p
8	152	76.8	200	19	W75958 Mouse cell surface
9	152	76.8	200	21	B08723 Amino acid sequenc
10	152	76.8	200	21	Y92212 Murine Th2-specific
11	152	76.8	120	15	R54669 Mouse brain natrin

12	7	3.5	120	15	R54670	Mouse brain natrin
13	7	3.5	170	3	P20107	Sequence encoded b
14	7	3.5	209	21	G14014	Arabidopsis thalia
15	7	3.5	209	21	G59943	Arabidopsis thalia
16	6	3.0	8	11	R08310	Histamine releasin
17	6	3.0	8	11	R81456	Histamine releasin
18	6	3.0	9	11	R08312	Histamine releasin
19	6	3.0	9	11	R08311	Histamine releasin
20	6	3.0	9	11	R81457	Histamine releasin
21	6	3.0	9	11	R81458	Histamine releasin
22	6	3.0	10	14	R37367	Group 6 synthetic
23	6	3.0	10	14	R37811	IgE - IgE Fc recep
24	6	3.0	10	15	R65358	IgE CH4 hapten - H
25	6	3.0	10	15	R52950	Mast cell chemical
26	6	3.0	10	16	R83187	IgE C-epsilon-4 co
27	6	3.0	10	17	R88818	IgE motif contg. p
28	6	3.0	10	17	R81455	Histamine releasin
29	6	3.0	10	17	R90708	Histamine releasin
30	6	3.0	10	18	W27058	Chemically synthe
31	6	3.0	10	18	W14426	Human IgE heavy ch
32	6	3.0	10	21	B20866	Immunoglobulin E e
33	6	3.0	10	21	B20876	Immunoglobulin E e
34	6	3.0	10	21	B80052	IgE derived target
35	6	3.0	10	22	B51040	IgE peptide #18.
36	6	3.0	11	17	R90709	Residues 496-506 o
37	6	3.0	11	17	B20877	Immunoglobulin E e
38	6	3.0	12	11	R08334	Histamine releasin
39	6	3.0	12	16	R82570	Human IgE CH4 regi
40	6	3.0	12	17	R81459	Histamine releasin
41	6	3.0	15	21	Y97275	Calycin conserved
42	6	3.0	22	14	R37812	H22V IgE - IgE Fc
43	6	3.0	22	18	W14427	Human IgE heavy ch
44	6	3.0	22	21	Y70332	Human gamma amino
45	6	3.0	24	16	R82600	IgE CH4 region con

#### ALIGNMENTS

RESULT 1	
ID Y92213	Y92213 standard; Protein: 198 AA.
XX AC Y92213:	
XX DT 10-AUG-2000	(first entry)
XX DE	Human Th2-specific polypeptide, h1228.
XX KW h1228; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;	
XX KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;	
XX KW antipsoriatic; antiallergic; anti-viral; optalmalological;	
XX KW CTLA-4; nephrotoxic; anti-HIV; antibacterial.	
OS Homo sapiens.	
XX FH	
XX FT Key	Location/Qualifiers
XX FT Peptide	113..118
XX FT	/label= conserved_ppp_motif
XX FT	/note= "common in CD28 and CTLA-4"
XX FT	178..181
XX FT Peptide	/label= YXXM_motif
XX FT	/note= "common in CD28 and CTLA-4; necessary for
XX FT	CD28-mediated phosphatidylinositol 3-kinase
XX FT	activity"
XX PR	
07-OCT-1998;	98US-0168229.
06-OCT-1999;	99WO-US23156.
13-APR-2000.	
MO200019988-A1.	

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PR 26-FEB-1999: 99US-0258670.
PR 06-OCT-1999: 99US-0413136.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
XX WPI: 2000-303619/26.
DR N-PSDB: A09056.
XX
PT T helper (Th) 2 nucleic acids and encoded proteins, useful for the
PT diagnosis and treatment of immune and respiratory disorders such as
PT Crohn's diseases, arthritis, insulin dependent diabetes and
PT autoimmunity
XX
XX Claim 16; Page 138-139; 159pp; English.
PS
XX
CC This Th2-specific polypeptide, which has similarity to human CD28 and
CC human CTLA-4 is encoded by human orthologue h1228.
CC A novel method for modulating a Th2 response, an immune response, or
CC suppressing airway inflammation or hyperresponsiveness in a mammal
CC comprising administering a Th2-specific polypeptide of the invention, an
CC antibody to such a polypeptide or allelic variants of the genes. The
CC novel DNA and polypeptide sequences are useful for treatment and
CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
CC viral infections (including human immunodeficiency virus (HIV)),
CC bacterial infections, bronchitis, cystic fibrosis, diphtheria,
CC emphysema, pneumonia, and Legionnaires disease.
CC
XX
SQ Sequence 198 AA:

Query Match 76.8%; Score 152; DB 21; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSGLMFFLECLRIKVTGGEINGSANYEMFIFHNGVQILCKYPDIVQCFKMLKGQ 60
DB 1 mksglwyfflfcrltkvltgelsanyemflfmgvqllckypdivqfkmqllkxgq 60
QY 61 ILCDLTKGSGNTVSIRSLKFCQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPFK 120
DB 61 ilcdltksgnsvtsirslkfcqslnnsvsfflynlshanyfcmstfdppfk 120
QY 121 VTLTGGLHYESQLCCQLKFWLPFGCAFYV 152
DB 121 vltlgylhyesqlccqlkfwlpgcaafyv 152

RESULT 2
W75956
ID W75956 standard; Protein: 199 AA.
XX
AC W75956;
XX
XX 11-DEC-1998 (first entry)
XX
XX Human cell surface protein #1.
XX
XX Human: cell surface protein; thymocyte; lymphocyte; cell adhesion;
XX signal transmission; autoimmune disorder; allergy; diagnosis;
XX mitogen-stimulated.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9838216-A1.
XX
XX PD 03-SEP-1998.
XX
XX PF 27-FEB-1998; 98WO-JP00837.

```

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XX
XX 26-FEB-1998; 98JP-0062217.
PR 27-FEB-1997; 97JP-0062290.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX Tamatani T, Tezuka K;
XX WPI: 1998-481144/41.
DR N-PSDB: V53198.
XX
XX Cell surface molecule expressed in thymocytes and lymphocytes and
XX mediating signal transmission and cell adhesion, and antibodies to
XX it useful in treatment of auto-immune and allergic disorders.
XX
XX Claim 2; Page 99-101; 149pp; Japanese.
PS
XX
CC The present sequence represents a human cell surface protein which is
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence RDPPEF in its extracellular region and the
CC sequence YMFN in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
CC
XX
SQ Sequence 199 AA:

Query Match 76.8%; Score 152; DB 19; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSGLMFFLECLRIKVTGGEINGSANYEMFIFHNGVQILCKYPDIVQCFKMLKGQ 60
DB 1 mksglwyfflfcrltkvltgelsanyemflfmgvqllckypdivqfkmqllkxgq 60
QY 61 ILCDLTKGSGNTVSIRSLKFCQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPFK 120
DB 61 ilcdltksgnsvtsirslkfcqslnnsvsfflynlshanyfcmstfdppfk 120
QY 121 VTLTGGLHYESQLCCQLKFWLPFGCAFYV 152
DB 121 vltlgylhyesqlccqlkfwlpgcaafyv 152

RESULT 3
W75957
ID W75957 standard; Protein: 199 AA.
XX
AC W75957;
XX
XX 11-DEC-1998 (first entry)
XX
XX Human cell surface protein #2.
XX
XX Human: cell surface protein; thymocyte; lymphocyte; cell adhesion;
XX signal transmission; autoimmune disorder; allergy; diagnosis;
XX mitogen-stimulated.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9838216-A1.
XX
XX PD 03-SEP-1998.
XX
XX PF 27-FEB-1998; 98WO-JP00837.
XX
XX PR 26-FEB-1998; 98JP-0062217.
XX
XX PR 27-FEB-1997; 97JP-0062290.

```

PA (NISB ) JAPAN TOBACCO INC.  
 XX  
 PI Tamatani T, Tezuka K;  
 XX  
 DR WPI; 1998-481144/41.  
 DR N-PSDB; V53199.  
 XX  
 PT Cell surface molecule expressed in thymocytes and lymphocytes and  
 PT mediating signal transmission and cell adhesion, and antibodies to  
 PT it useful in treatment of auto-immune and allergic disorders.  
 XX  
 PS Claim 9; Page 101-105; 149pp; Japanese.  
 CC  
 CC The present sequence represents a human cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognising the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains  
 CC the amino acid sequence FPPPPF in its extracellular region and the  
 CC sequence YMFH in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of auto-immune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.  
 CC  
 XX  
 SQ Sequence 199 AA:  
 Query Match 76.8%; Score 152; DB 19; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMSGIWFPLFLRLIKVLTEINGSNANYEMFTFHNGVQIICKYDPIVOQFMQLKGGQ 60  
 Db 1 mmsgiwyfflfcrlrlkvltgelngsanymftfhngvqilckypdivqfkmqlkqg 60  
 QY 61 IICDLTKRKSGNTWSIKSLKFCCHSOLSNNSVSFPLYNDHSHANYFCNLSIFDPPPK 120  
 Db 61 iicdltkrksgntwsi kslkfcchsqslsnsvsfplyndhshanyfcnl sifdpppk 120  
 QY 121 VPLTGGYLHYESQLCCOLKFWLPITGCAAFV 152  
 Db 121 vpltggylyhyesqlccqlkfwlpigcaafv 152  
 RESULT 4  
 26  
 Y08026 standard; Protein: 199 AA.  
 XX  
 AC Y08026;  
 XX  
 DT 08-JUL-1999 (first entry)  
 XX  
 DE Human activated T-lymphocyte protein 8F4.  
 XX  
 KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;  
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;  
 KW T cell activation; cytokine synthesis; regulatory element; B cell;  
 KW T cell-dependent antibody production; treatment; prevention; cancer;  
 KW autoimmune disease; transplant rejection; immune system regulation;  
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09915553-A2.  
 XX  
 PD 01-APR-1999.  
 XX  
 PF 23-SEP-1998; 98MO-DE02896.  
 XX  
 PR 11-MAY-1998; 98DE-1021060.  
 PR 23-SEP-1997; 97DE-1041929.  
 XX  
 PA (DEKO-) DEUT KOCH INST ROBERT:

PA (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.  
 XX  
 PI KroczeK R;  
 XX  
 DR WPI; 1999-276975/23.  
 DR N-PSDB; X37661.  
 XX  
 PT Polypeptide 8F4 co-stimulates T cells and is present only on  
 PT activated cells  
 XX  
 PS Claim 2; Page 24; 47pp; German.  
 CC  
 CC This invention describes a novel human protein, 8F4, and its encoding  
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+  
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,  
 CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,  
 CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a  
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies  
 CC proliferation of T cells, synthesis of certain cytokines and other  
 CC regulatory agents, and improves T cell-dependent antibody production  
 CC by B cells. Agents that inhibit 8F4 are used to treat or prevent  
 CC autoimmune diseases, to prevent transplant rejection and to treat  
 CC disorders of immune system regulation. 8F4, or cells that express it,  
 CC is/are used to treat or prevent cancers, acquired immune deficiency  
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).  
 CC  
 XX  
 SQ Sequence 199 AA:  
 Query Match 76.8%; Score 152; DB 20; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMSGIWFPLFLRLIKVLTEINGSNANYEMFTFHNGVQIICKYDPIVOQFMQLKGGQ 60  
 Db 1 mmsgiwyfflfcrlrlkvltgelngsanymftfhngvqilckypdivqfkmqlkqg 60  
 QY 61 IICDLTKRKSGNTWSIKSLKFCCHSOLSNNSVSFPLYNDHSHANYFCNLSIFDPPPK 120  
 Db 61 iicdltkrksgntwsi kslkfcchsqslsnsvsfplyndhshanyfcnl sifdpppk 120  
 QY 121 VPLTGGYLHYESQLCCOLKFWLPITGCAAFV 152  
 Db 121 vpltggylyhyesqlccqlkfwlpigcaafv 152  
 RESULT 5  
 B08731  
 B08731 standard; Protein: 199 AA.  
 XX  
 AC B08731;  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human CRP1 polypeptide.  
 XX  
 KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;  
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;  
 KW T cell proliferation; T-cell mediated disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH Peptide  
 FT 1..20 Location/Qualifiers  
 FT /note="signal peptide"  
 FT 21..199  
 FT Protein /note="mature protein"  
 FT 21..140  
 FT Domain /note="extracellular domain"  
 FT 141..161  
 FT Domain /note="predicted transmembrane domain"  
 FT 162..199  
 FT Domain /note="intracellular domain"

[illegible]

```

PF 27-FEB-1998; 98WO-JP00837.
XX
PR 26-FEB-1998; 98JP-0062217.
PR 27-FEB-1997; 97JP-0062290.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
PI Tamatani T, Tezuka K;
XX
DR WPI: 1998-481144/41.
DR N-PSDB; V61357.
XX
PT Cell surface molecule expressed in thymocytes and lymphocytes and
PT mediating signal transmission and cell adhesion, and antibodies to
PT it useful in treatment of auto-immune and allergic disorders.
XX
PS Claim 9; Page 106-109; 149pp; Japanese.
XX
CC The present sequence represents a rat cell surface protein which is
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence FDDPPF in its extracellular region and the
CC sequence YMFV in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
XX
SO Sequence 200 AA;

Query Match 8.6%; Score 17; DB 19; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LCDLTKTKGSGNTVSIR 78
   |||||||
DB 62 LCDLTKKSGNTVSIK 78

RESULT 7
W71875
ID W71875 standard; Protein; 216 AA.
XX
AC W71875;
XX
DT 11-DEC-1998 (first entry)
XX
DE Rat cell surface protein #2.
XX
KW Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW signal transmissiion; autoimmune disorder; allergy; diagnosis;
KW mitogen-stimulated.
XX
OS Rattus sp.
XX
PN W09838216-A1.
XX
PD 03-SEP-1998.
XX
PF 27-FEB-1998; 98WO-JP00837.
XX
PR 26-FEB-1998; 98JP-0062217.
PR 27-FEB-1997; 97JP-0062290.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
PI Tamatani T, Tezuka K;
XX
DR WPI: 1998-481144/41.
DR N-PSDB; V61358.
XX

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PT Cell surface molecule expressed in thymocytes and lymphocytes and  
 PT mediating signal transmission and cell adhesion, and antibodies to  
 PT it useful in treatment of auto-immune and allergic disorders.

PS Claim 9; Page 112-115; 149pp; Japanese.

CC The present sequence represents a rat cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognising the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains  
 CC the amino acid sequence FDDPPF in its extracellular region and the  
 CC sequence YMFH in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of auto-immune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.

Sequence 216 AA:

Query Match 8.6%; Score 17; DB 19; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LCDLTKRGSGMTVSIK 78  
 ||||||||||||||||  
 DB 62 LCDLTKRGSGMTVSIK 78

RESULT 8  
 W75958  
 ID W75958 standard; Protein; 200 AA.

AC W75958;  
 XX  
 DT 11-DEC-1998 (first entry)

DE Mouse cell surface protein.

KM Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion;  
 KM signal transmission; auto-immune disorder; allergy; diagnosis;  
 KM mitogen-stimulated.

OS Mus sp.

WO9838216-A1.

PD 03-SEP-1998.

PF 27-FEB-1998; 98WO-JP00837.

PR 26-FEB-1998; 98JP-0062217.

PR 27-FEB-1997; 97JP-0062290.

PA (NISH) JAPAN TOBACCO INC.

PI Tamatani T, Tezuka K;

WI: 1998-481144/41.

DR N-PSDB; V53200.

PT Cell surface molecule expressed in thymocytes and lymphocytes and  
 PT mediating signal transmission and cell adhesion, and antibodies to  
 PT it useful in treatment of auto-immune and allergic disorders.

PS Claim 9; Page 110-112; 149pp; Japanese.

CC The present sequence represents a mouse cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognising the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains

CC the amino acid sequence FDDPPF in its extracellular region and the  
 CC sequence YMFH in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of auto-immune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.

SO Sequence 200 AA;

Query Match 8.1%; Score 16; DB 19; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 125 GGYIHYESQLCCQK 140  
 ||||||||||||||||  
 DB 126 GGYIHYESQLCCQK 141

RESULT 9  
 B08723  
 ID B08723 standard; Protein; 200 AA.

AC B08723;

DT 02-JAN-2001 (first entry)

DE Amino acid sequence of a murine CRP1 polypeptide.

KM CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;

KM T-lymphocyte activation; type I transmembrane protein; T cell activation;  
 KM T cell proliferation; T-cell mediated disorder.

OS Mus sp.

Location/Qualifiers  
 FT Key 1..20  
 FT Peptide /note= "signal peptide"  
 FT Protein 21..200  
 FT /note= "mature protein"  
 FT Domain 21..145  
 FT /note= "extracellular domain"  
 FT Domain 146..163  
 FT /note= "predicted transmembrane domain"  
 FT Domain 164..200  
 FT /note= "intracellular domain"

WO200046240-A2.

PN 10-AUG-2000.

PF 27-JAN-2000; 2000WO-US01871.

PR 03-FEB-1999; 99US-0244448.

PR 08-MAR-1999; 99US-0264527.

PA (AMGE-) AMGEN INC.

PI Yoshinaga SK;

WI: 2000-543476/49.

DR N-PSDB; A64554.

PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful  
 PT in the treatment, prevention and diagnosis of T cell mediated disorders

PS Claim 11; Fig 1A; 174pp; English.

CC The present sequence represents a CRP1 (CD28 related protein-1)  
 CC polypeptide. The specification also describes a B7RP1 (B7 related  
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte  
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are  
 CC predicted to be a type I transmembrane protein. The nucleic acids are  
 CC useful for regulating T cell activation or proliferation in an animal.

CC The polypeptides are useful for treating, preventing ameliorating or  
CC diagnosing a T-cell mediated disorder in an animal. They can also be  
CC used to identify test molecules that bind to the polypeptides.  
XX

SO Sequence 200 AA;

Query Match 8.1%; Score 16; DB 21; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLHIYESQLCCQLK 140  
Db 126 ggyLhiyesqlccqLk 141

RESULT 10  
Y92212  
ID Y92212 standard; Protein; 200 AA.  
XX  
AC Y92212;  
XX  
F 10-AUG-2000 (first entry)  
XX

DE Murine Th2-specific polypeptide, m1228.

XX m1288; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;  
KM CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;  
KM antipsoriatic; antiallergic; antiviral; ophthalmological;  
KM CTLA-4; nephrotoxic; anti-HIV; antibacterial.  
XX  
OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 114..119  
FT /label="conserved\_PPP\_motif  
FT /note="common in CD28 and CTLA-4"  
FT 181..184  
FT /label="YXXM\_motif  
FT /note="common in CD28 and CTLA-4; necessary for  
FT CD28-mediated phosphatidylinositol 3-kinase  
FT activity"  
XX

PN WC0200019988-A1.

PD 13-APR-2000.

PF 06-OCT-1999; 99WO-US23156.

XX 07-OCT-1998; 98US-0168229.

PR 26-FEB-1999; 99US-0258670.

XX 06-OCT-1999; 99US-0413136.

XX (MILL-) MILLENNIUM PHARM INC.

PA Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;

PI WPI: 2000-303619/26.

DR N-PSDB; A09054.

XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the  
PT diagnosis and treatment of immune and respiratory disorders such as  
PT Crohn's diseases, arthritis, insulin dependent diabetes and  
PT autoimmunity  
XX

PS Claim 16; Page 130-131; 159pp; English.

XX This Th2-specific polypeptide is encoded by a murine orthologue m1288.

CC The protein shares homology with both human and murine CD28 and CTLA-4.

CC A novel method for modulating a Th2 response, an immune response, or  
CC suppressing airway inflammation or hyperresponsiveness in a mamma

CC comprises administering a Th2-specific polypeptide of the invention, an  
CC antibody to such a polypeptide or allelic variants of the genes. The

CC novel DNA and polypeptide sequences are useful for treatment and  
CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,  
CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,  
CC dermatitis, psoriasis, graft rejection, graft versus host diseases,  
CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,  
CC viral infections (including human immunodeficiency virus (HIV)),  
CC bacterial infections, bronchitis, cystic fibrosis, diphtheria,  
CC emphysema, pneumonia, and Legionnaires disease.  
XX

SO Sequence 200 AA;

Query Match 8.1%; Score 16; DB 21; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLHIYESQLCCQLK 140  
Db 126 ggyLhiyesqlccqLk 141

RESULT 11

R54669  
ID R54669 standard; Protein; 120 AA.

XX R54669;

DT 12-JAN-1995 (first entry)

DE Mouse brain natriuretic peptide.

XX Brain natriuretic peptide; BNP; detection.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..75  
FT /label="sig\_peptide  
FT 76..120  
FT /label="mat\_protein  
FT Region 1..120  
FT /note="Met(-75)-Leu(45); claim 5"  
FT 26..120  
FT /note="Ser(-50)-Leu(45); claim 4"  
FT Region  
XX

PN JP06107688-A.

PD 19-APR-1994.

PF 29-SEP-1992; 92JP-0259488.

XX 29-SEP-1992; 92JP-0259488.

XX (SHIO ) SHIONOGI & CO LTD.

PA WPI: 1994-163940/20.

DR N-PSDB; Q65357.

XX Mouse brain natriuretic peptide - useful for the detection and  
PT determination of BNP

PS Disclosure; Page 7-8; 9pp; Japanese.

XX Mouse BNP can be used for the detection and the determination  
CC of BNP in a sample and for the prepn. of various reagents contg.

CC BNP.

XX Sequence 120 AA;

Query Match 3.5%; Score 7; DB 15; Length 120;

Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 QFKMQLL 56  
 DB 38 qfkmqll 44

## RESULT 12

RS4670  
 ID RS4670 standard; Protein: 120 AA.

AC RS4670;

DT 12-JAN-1995 (first entry)

DE Mouse brain natriuretic peptide.

XX Brain natriuretic peptide; BNP; detection.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..75  
 FT /label= sig\_peptide

FT Protein 76..120  
 FT /label= mat\_protein

PN JP06107688-A.

PD 19-APR-1994.

PE 29-SEP-1992; 92JP-0259488.

PR 29-SEP-1992; 92JP-0259488.

PA (SHIO ) SHIONOGI & CO LTD.

XX MPI: 1994-163940/20.

DR N-PSDB; Q65358.

PT Mouse brain natriuretic peptide - useful for the detection and

PS determination of BNP

XX Disclosure; Page 8-9; 9pp; Japanese.

CC Mouse BNP can be used for the detection and the determination

XX of BNP in a sample and for the prepn. of various reagents contg.

XX BNP.

XX Sequence 120 AA;

Query Match 3.5%; Score 7; DB 15; Length 120;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 QFKMQLL 56

DB 38 qfkmqll 44

## RESULT 13

RS4670  
 ID P20107 standard; Protein: 170 AA.

AC P20107;

DT 10-AUG-1992 (first entry)

DE Sequence encoded by leukocyte interferon leif E cDNA.

XX Viral infection; therapy; malignancy.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Peptide 1..4  
 FT /label= signal

PN GB2079291-A.

PD 20-JAN-1992.

PE 01-JUL-1981; 81GB-0120279.

PR 21-APR-1981; 81US-0256204.

PR 01-JUL-1980; 80US-0164986.

PR 08-SEP-1980; 80US-0184909.

PR 10-NOV-1980; 80US-0205578.

PA (HOFF ) HOFFMANN-LA ROCHE AG.

XX (GENE-) GENENTECH INC.

PI Goeddel DYN, Pestka S;

DR MPI: 1982-04460E/03.

DR N-PSDB; N20094.

XX Mature human leukocyte interferon polypeptide(s) - prepd. from

PT microdes transformed with appropriate DNA sequences

PS Example; Fig 4; 20pp; English.

CC The inventors claim a polypeptide comprising the AA sequence of a

CC mature human leif and a DNA sequence encoding it. Leif A-D, F, H-J

CC and encoding DNA are specifically claimed. They are natural allelic

CC variations. Leif is isolated from the leukocytes of humans with

CC chronic myelogenous leukemia, induced to produce interferon with

CC Sendai or Newcastle disease virus; esp. the cell line KG-1.

XX Sequence 170 AA;

Query Match 3.5%; Score 7; DB 3; Length 170;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 LTKKKYS 169

DB 135 ltkkys 141

## RESULT 14

RS4670  
 ID G14014 standard; Protein: 209 AA.

AC G14014;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 13719.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 24-JUN-1999; 99US-0140695.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142820.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148584.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0152363.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155186.  
PR 24-SEP-1999; 99US-0156559.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157153.  
PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
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PR 21-OCT-1999; 99US-0160767.  
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PR 21-OCT-1999; 99US-0160811.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 3.5%; Score 7; DB 21; Length 209;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YFFFLCL 13  
|||||  
Db 67 yffflcl 73

RESULT 15  
G59943  
ID G59943 standard; Protein; 209 AA.  
XX  
G59943;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 77591.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hydrolisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.  
EP1033405-A2.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 23-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130049.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131048.  
PR 30-APR-1999; 99US-0132049.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139817.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147316.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151338.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.

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PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160880.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 3.5%; Score 7; DB 21; Length 209;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YFFPFL 13  
Db 67 yfflcl 73

Search completed: May 30, 2001, 16:52:29  
Job time: 25 sec

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:04 ; Search time 14.15 Seconds

(without alignments)  
961.635 Million cell updates/sec

Title: us-09-509-283-2

Perfect score: 198

Sequence: 1 MKSGLMYFFFLCRLKRVKLG.....YMPRAVNTAKKSLRDVTL 198

Scoring table: OLIGO

Gapop: 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	76.8	199	2	inducible T-cell c
2	17	8.6	200	2	activation-inducib
3	17	8.6	216	2	antibiotic resista
4	8	4.0	261	2	ribosomal protein
5	7	3.5	147	1	hypothetical prote
6	7	3.5	209	2	phosphoglycolate p
7	7	3.5	221	2	probable n-acetyl
8	7	3.5	276	2	proline-rich prote
9	7	3.5	385	2	translation elonga
10	7	3.5	513	2	conserved hypothet
11	7	3.5	558	2	hypothetical prote
12	7	3.5	605	2	inter-alpha-trypsi
13	7	3.5	907	2	probable translati
14	7	3.5	1047	2	hypothetical prote
15	7	3.5	1291	2	S-layer protein -
16	7	3.5	1361	2	ATP-binding cassel
17	7	3.5	1466	2	14k protein - pea
18	7	3.5	1766	2	groovin gene proce
19	7	3.5	4151	2	hypothetical prote
20	6	3.0	32	2	ribosomal protein
21	6	3.0	72	2	M-like protein emn
22	6	3.0	82	2	hypothetical prote
23	6	3.0	85	2	single strand DNA-
24	6	3.0	98	2	probable transpos
25	6	3.0	99	2	Ig epsilon chain C
26	6	3.0	99	2	hypothetical CRF-1
27	6	3.0	100	2	serotonin receptor
28	6	3.0	102	2	T-cell receptor al
29	6	3.0	110	2	JH0334

30	6	3.0	113	2	549981	Tcell receptor alp
31	6	3.0	113	2	725658	hypothetical prote
32	6	3.0	115	2	E53116	Ig epsilon chain C
33	6	3.0	121	2	T24096	hypothetical prote
34	6	3.0	126	2	C53116	Ig epsilon chain C
35	6	3.0	129	2	T50446	conserved hypothet
36	6	3.0	130	2	S67024	probable membrane
37	6	3.0	135	2	E71413	ribosomal protein
38	6	3.0	135	2	T06426	ribosomal protein
39	6	3.0	135	2	T06430	ribosomal protein
40	6	3.0	135	2	T06431	ribosomal protein
41	6	3.0	135	2	T06451	ribosomal protein
42	6	3.0	135	2	B70456	thioredoxin - Aqu
43	6	3.0	138	2	E81045	hypothetical prote
44	6	3.0	150	2	D46036	galactosyltransfer
45	6	3.0	153	2	B69033	conserved hypothet

#### ALIGNMENTS

```

RESULT 1
S78540
Inducible T-cell co-stimulator ICOS precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999
C:Accession: S78540; S78748; S78749
R:Kroczek, R.
submitted to the Protein Sequence Database, June 1998
A:Reference number: S78540
A:Accession: S78540
A:Molecule type: mRNA
A:Residues: 1-199 <KRO>
A:Experimental source: cell line MOLT-4V
R:Hutloff, A.; Dittlich, A.M.; Beler, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop
Nature 397, 263-266, 1999
A:title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela
A:Reference number: S78748; MUID:99127892
A:Accession: S78748
A:Molecule type: mRNA
A:Residues: 1-199 <HUT1>
A:Experimental source: cell line MOLT-4V
A:Accession: S78749
A:Molecule type: protein
A:Residues: 'X', 193-198 <HUT2>
A:Experimental source: cell line MOLT-4V
C:Complex: homodimer
C:Superfamily: immunoglobulin homology
C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein
F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>
F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT>
F:21-138/Domain: extracellular #status predicted <EXT>
F:26-132/Domain: immunoglobulin homology <IMM>
F:139-164/Domain: transmembrane #status predicted <TM>
F:165-199/Domain: intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match          76.8%; Score 152; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 2,1e-155;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	MKSGLMYFFFLCRLKRVLTGEINGSNYMFTHNGGVQILCKYPDIYVOQFMQLKGGQ	60
DB	1	MKSGLMYFFFLCRLKRVLTGEINGSNYMFTHNGGVQILCKYPDIYVOQFMQLKGGQ	60
QY	61	ILCDLTKTKGSGNTVSIRKSLKCHSOLSNNSVSFLYXNDHSHANYFCNLSTPDPPEK	120
DB	61	ILCDLTKTKGSGNTVSIRKSLKCHSOLSNNSVSFLYXNDHSHANYFCNLSTPDPPEK	120
QY	121	VLTGGLHYEISQLCCQLKFWLPTGCAFAVV	152
DB	121	VLTGGLHYEISQLCCQLKFWLPTGCAFAVV	152

RESULT 2  
JC7397  
activation-inducible lymphocyte immuno-mediatory molecule-2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 17-Nov-2000  
C:Accession: JC7397; PC7100  
R:Rezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, B.; Bloch, R.; Res. Commun. 276, 335-345, 2000  
A:Title: Identification and characterization of rat AILM/ICOS, a novel T-cell costimulatory molecule  
A:Reference number: JC7396  
A:Contents: Spleen  
A:Accession: JC7397  
A:Molecule type: mRNA  
A:Residues: 1-200 <TEZ>  
A:Cross-references: DDBJ:AB023134  
A:Accession: PC7100  
A:Molecule type: protein  
A:Residues: 21-40 <TEZ>  
C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.  
C:Genetics:  
C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 8.6%; Score 17; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LCDLTKTKSGNTVSIK 78  
|||||  
Db 62 LCDLTKTKSGNTVSIK 78

RESULT 3  
JC7396  
activation-inducible lymphocyte immuno-mediatory molecule-1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 17-Nov-2000  
C:Accession: JC7396; PC7099  
R:Rezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, B.; Bloch, R.; Res. Commun. 276, 335-345, 2000  
A:Title: Identification and characterization of rat AILM/ICOS, a novel T-cell costimulatory molecule  
A:Reference number: JC7396  
A:Contents: Spleen  
A:Accession: JC7396  
A:Molecule type: mRNA  
A:Residues: 1-216 <TEZ>  
A:Cross-references: DDBJ:AB023133  
A:Accession: PC7099  
A:Molecule type: protein  
A:Residues: 21-40 <TEZ>  
C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.  
C:Genetics:  
A:Gene: ailm-1  
C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 8.6%; Score 17; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 2.3e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LCDLTKTKSGNTVSIK 78  
|||||  
Db 62 LCDLTKTKSGNTVSIK 78

RESULT 4  
H69779  
antibiotic resistance protein homolog ydfB - Bacillus subtilis

C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: H69779  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: H69779  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber A.; Ehlich, S.D.; Emmertson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gal lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M Koeter, P.; Konigsdorf, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A:Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akewich, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis  
A:Reference number: A69580; M01D:98044033  
A:Accession: H69779  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-261 <KUN>  
A:Cross-references: GB:299106; GB:AL009126; NID:q2632653; PIDN:CAB12342.1; PID:q26328 A:Experimental source: strain 168  
C:Genetics:  
A:Gene: ydfB  
C:Superfamily: probable antibiotic resistance protein ydfB

Query Match 4.0%; Score 8; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 LTKKKYSS 170  
|||||  
Db 7 LTKKKYSS 14

RESULT 5  
RHS12  
ribosomal protein S19, er [validated] - Halocaula marismortui  
N:Alternate names: ribosomal protein E1.3; ribosomal protein HS12  
C:Species: Halocaula marismortui  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 04-Feb-2000  
C:Accession: S00183; C24304  
R:Kimura, J.; Arndt, E.; Kimura, M.  
FEBS Lett. 224, 65-70, 1987  
A:Title: Primary structures of three highly acidic ribosomal proteins S6, S12 and S15  
A:Reference number: S00182; M01D:88055606  
A:Accession: S00183  
A:Molecule type: protein  
A:Residues: 1-147 <KIM>  
A:Note: the source is designated as Halobacterium marismortui  
R:Shoem, M.; Dijk, J.; Reinhardt, R.; Wiltmann-Liebold, B.  
FEBS Lett. 204, 323-330, 1986  
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit  
A:Reference number: A24304  
A:Accession: C24304  
A:Molecule type: protein  
A:Residues: 1-11, 'E', '13-14, 'T', '16-18, 'T', '20-21 <SHO>  
A:Note: the source is designated as Halobacterium marismortui  
C:Superfamily: rat ribosomal protein S19  
C:Keywords: protein biosynthesis; ribosome

Query Match 3.5%; Score 7; DB 1; Length 147;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 KTKGSGN 73  
|||||



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## OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:49 ; Search time 9.63 Seconds  
(without alignments) 704.318 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198  
Sequence: 1 MKSGIMYFFLFCRLRKVLTG.....YMFRAVNTAKSRSLTDVTL 198

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	3.5	147	1	R19E_HALMA
2	7	3.5	907	1	ITH1_MOUSE
3	6	3.0	72	1	RL28_THEMA
4	6	3.0	100	1	NUIM_PHEIN
5	6	3.0	121	1	ITHL_CAEL
6	6	3.0	135	1	RL27_ARATH
7	6	3.0	139	1	RL27_PEA
8	6	3.0	139	1	RPB6_ASFEM2
9	6	3.0	147	1	RPB6_ASFEM2
10	6	3.0	160	1	FMA3_ECOLI
11	6	3.0	160	1	FMA3_ECOLI
12	6	3.0	179	1	FMDR_ECOLI
13	6	3.0	179	1	YAIL_ECOLI
14	6	3.0	186	1	YFCP_ECOLI
15	6	3.0	189	1	YCEB_ECOLI
16	6	3.0	189	1	BBP_PIEBR
17	6	3.0	191	1	RPOE_HAETIN
18	6	3.0	191	1	RI9A_YEAST
19	6	3.0	191	1	RI9B_YEAST
20	6	3.0	191	1	RPOE_ECOLI
21	6	3.0	214	1	RNS2_SALT
22	6	3.0	237	1	Y450_MYCPN
23	6	3.0	240	1	NESA_ECOLI
24	6	3.0	241	1	YMO8_PARTE
25	6	3.0	247	1	TRY4_RAT
26	6	3.0	248	1	TRY4_RAT
27	6	3.0	262	1	YHUF_ECOLI
28	6	3.0	274	1	YALC_SCHPO
29	6	3.0	286	1	ISPE_BUCAI
30	6	3.0	287	1	RN07_SCHPO
31	6	3.0	291	1	SFAH_ECOLI
32	6	3.0	304	1	CAHH_VACCC
33	6	3.0	304	1	CAHH_VACCV

34	6	3.0	304	1	CAHH_VARY	P33065 variola vir
35	6	3.0	306	1	RCHEM_RHOCA	P11847 rhododact
36	6	3.0	307	1	RCHEM_RHOSH	P02953 rhododact
37	6	3.0	313	1	NU2M_RHISA	P09817 rhipechal
38	6	3.0	320	1	YB9K_YEAST	P38342 saccharomyc
39	6	3.0	324	1	MAS_MOUSE	P30554 mus musculu
40	6	3.0	324	1	MAS_RAT	P12526 rattus norv
41	6	3.0	343	1	FPPS_ARTAN	P49350 artemisia a
42	6	3.0	346	1	YC54_SYNY3	P74078 synecocyst
43	6	3.0	356	1	KARG_SCHAM	P91798 schistocerc
44	6	3.0	358	1	GLPO_ECOLI	P09394 escherichia
45	6	3.0	359	1	ODPB_PEA	P52904 pisum sativ

## ALIGNMENTS

RESULT 1	
ID R19E_HALMA	STANDARD: PRT: 147 AA.
AC P19952:	
DT 01-FEB-1991 (Rel. 17, Created)	
DT 01-FEB-1991 (Rel. 17, Last sequence update)	
DT 30-MAY-2000 (Rel. 39, Last annotation update)	
DE 30S RIBOSOMAL PROTEIN S19E (HS12) (EI.3).	
GN RPS19E.	
OS Haloarcula marismortui (Haloaracterium marismortui).	
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.	
OX NCBI_TaxID=2238;	
RN [1]	
RP SEQUENCE.	
RX MEDLINE=86055606; PubMed=3315748;	
RA Kimura J., Arndt E., Kimura M.;	
RT "Primary structures of three highly acidic ribosomal proteins S6, S12 and S15 from the archaebacterium Halobacterium marismortui.";	
RL FEBS Lett. 224:65-70(1987).	
RN [2]	
RP SEQUENCE OF 1-21.	
RA Shoham M., Dijk J., Reinhardt R., Wiltmann-Liebold B.;	
RT "Purification and characterization of ribosomal proteins from the 30S subunit of the extreme halophile Halobacterium marismortui.";	
RL FEBS Lett. 204:323-330(1986).	
CC -1- SIMILARITY: BELONGS TO THE S19E FAMILY OF RIBOSOMAL PROTEINS.	
DR PIR: S00183; R3HS12.	
DR InterPro: IPR001266; ..	
DR Pfam: PF01090; Ribosomal_S19e; 1.	
DR PROSITE: PS00628; RIBOSOMAL_S19E; 1.	
KW Ribosomal protein.	
FT CONFLICT 12 I -> E (IN REF. 2).	
FT CONFLICT 15 L -> I (IN REF. 2).	
FT CONFLICT 19 L -> I (IN REF. 2).	
SO SEQUENCE 147 AA; 16438 MW; 8F66327D14530FE CRC64;	
Query Match	3.5%; Score 7; DB 1; Length 147;
Best Local Similarity	100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY 67 KTKGSGN 73	
DB 87 KTKGSGN 93	
RESULT 2	
ID ITH1_MOUSE	STANDARD: PRT: 907 AA.
AC O61702:	
DT 15-JUL-1998 (Rel. 36, Created)	
DT 15-JUL-1998 (Rel. 36, Last sequence update)	
DT 01-OCT-2000 (Rel. 40, Last annotation update)	
DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 PRECURSOR (ITI HEAVY CHAIN H1).	
GN ITH1.	

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6N; TISSUE=Liver;  
 RX MEDLINE=95194326; PubMed=7534067;  
 RA Chan P., Risler J.-L., Raguenez G., Sallier J.-P.;  
 RT "The three heavy-chain precursors for the inter-alpha-inhibitor family  
 in mouse: new members of the multicopper oxidase protein group with  
 differential transcription in liver and brain";  
 RL Biochem. J. 306:505-512(1995).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 WFMA DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X70391; CAA49841.1; -  
 CC MGD: MGI:96618; Itih1.  
 CC DR InterPro: IPR002035; -  
 CC DR Pfam: PF00092; wfa\_1.  
 CC DR PROSITE: PS50234; WFMA\_DOMAIN; 1.  
 CC KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 CC Glycoprotein.  
 CC FT SIGNAL 1 26  
 CC FT CHAIN 27 668  
 CC FT POTENTIAL.  
 CC FT INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
 CC FT H1  
 CC FT PROPER 669 907  
 CC FT DOMAIN 287 447  
 CC FT CARBOHYD 282 282  
 CC FT CARBOHYD 285 285  
 CC FT CARBOHYD 585 585  
 CC FT BINDING 668 668  
 CC FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
 CC FT (BY SIMILARITY).  
 CC SO SEQUENCE 907 AA; 101082 MW; FE7FD76500CAF3BC CRC64;  
 CC -----  
 CC Query Match 3.5%; Score 7; DB 1; Length 907;  
 CC Best Local Similarity 100.0%; Pred. No. 20;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC QY 75 VSIRSLK 81  
 CC ID 1111111  
 CC DB 48 VSIRSLK 54  
 CC -----  
 CC RESULT 3  
 CC RL28\_THEME STANDARD; PRT; 72 AA.  
 CC ID RL28\_THEME  
 CC AC 09WY96;  
 CC DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE 50S RIBOSOMAL PROTEIN L28.  
 GN RPB8 OR TM0255.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogales; Thermotoga.  
 OX NCBI\_TaxID=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB / DSM 3109;  
 RX MEDLINE=99287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Liner K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of Thermotoga maritima";  
 RL Nature 399:323-329(1999).  
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AE001708; AAD35344.1; -  
 CC DR TIGR: TM0255; -  
 CC DR InterPro: IPR001383; -  
 CC DR Pfam: PF00830; Ribosomal\_L28; 1.  
 CC KW Ribosomal protein.  
 CC SO SEQUENCE 72 AA; 8052 MW; A18B09B0F9F76B49 CRC64;  
 CC -----  
 CC Query Match 3.0%; Score 6; DB 1; Length 72;  
 CC Best Local Similarity 100.0%; Pred. No. 26;  
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC QY 71 SGNVTS 76  
 CC ID 1111111  
 CC DB 16 SGNVTS 21  
 CC -----  
 CC RESULT 4  
 CC NULM\_PHYIN STANDARD; PRT; 100 AA.  
 CC ID NULM\_PHYIN  
 CC AC Q37598;  
 CC DT 15-JUL-1998 (Rel. 36, Created)  
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 CC DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 CC DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).  
 CC GN ND4L OR NAD4L.  
 CC OS Phytochthora infestans (Potato late blight fungus).  
 CC OS Mitochondrion.  
 CC OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
 CC Pytophthora.  
 CC OX NCBI\_TaxID=4787;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=ATCC 16981;  
 CC RA Chesnick J.M., Tuxbury K., Coleman A., Burger G., Lang B.F.;  
 CC Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -- NAD(+) + UBIQUINOL.  
 CC -----  
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:34 ; Search time 22.71 Seconds

(without alignments)  
1021.892 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198  
Sequence: 1 MMSGLWFFFLFCLRIKRVLTG.....YMFRAVNTAKKSRLTDTVTL 198

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL.15:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	76.8	199	4	O9Y6W8
2	152	8.6	200	11	O9R1T7
3	17	8.6	216	11	O9WVR9
4	16	8.1	200	11	O9WVS0
5	16	8.1	200	11	O9JUL7
6	8	4.0	261	2	P96679
7	8	4.0	1243	2	O9RDS5
8	4	3.5	108	5	O9V7Z6
9	7	3.5	173	9	O38610
10	7	3.5	209	10	O9SWC9
11	7	3.5	221	2	P73525
12	7	3.5	309	14	O72512
13	7	3.5	309	14	O71309
14	7	3.5	359	13	O9IBP8
15	7	3.5	385	14	O41160
16	7	3.5	387	13	O9IBG0
17	7	3.5	471	14	O84697
18	7	3.5	513	3	O9UUL5
19	7	3.5	549	5	O24204

20	7	3.5	558	2	O9PKV6	O9PKV6 chlamydia m
21	7	3.5	605	2	O83607	O83607 treponema p
22	7	3.5	817	5	O9VZJ5	O9VZJ5 drosophila
23	7	3.5	962	3	O14437	O14437 uromyces fa
24	7	3.5	997	3	O74242	O74242 cryptococcus
25	7	3.5	998	3	O9UR20	O9UR20 cryptococcus
26	7	3.5	1047	3	O94489	O94489 schizosacch
27	7	3.5	1152	4	O9NUF2	O9NUF2 homo sapien
28	7	3.5	1291	10	O9SU54	O9SU54 arabidopsis
29	7	3.5	1319	4	O94885	O94885 homo sapien
30	7	3.5	1361	2	O30524	O30524 wolimella r
31	7	3.5	1361	2	O87083	O87083 wolimella r
32	7	3.5	1466	3	P78576	P78576 emericella
33	7	3.5	1766	14	O9WJD8	O9WJD8 pea early b
34	7	3.5	4151	5	O96936	O96936 drosophila
35	7	3.5	4625	10	O9SMH3	O9SMH3 chlamydomon
36	7	3.5	5201	5	O9U479	O9U479 drosophila
37	7	3.5	5293	5	O9V6V2	O9V6V2 drosophila
38	7	3.5	5385	5	O9V6V3	O9V6V3 drosophila
39	6	3.0	32	2	O50861	O50861 borrelia bu
40	6	3.0	79	2	O9X9G0	O9X9G0 yersinia ps
41	6	3.0	79	14	O04252	O04252 human papil
42	6	3.0	82	2	O54656	O54656 streptococc
43	6	3.0	87	2	O55319	O55319 streptococc
44	6	3.0	92	14	O9JEN0	O9JEN0 human immun
45	6	3.0	93	10	O9SQW7	O9SQW7 arabidopsis

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	199 AA.
O9Y6W8	O9Y6W8			
AC	O9Y6W8			
DT	01-NOV-1999 (TREMBlrel. 12, Created)			
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)			
DE	ACTIVATOR-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM			
DE	PRECUSOR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BLOOD;			
RA	Tezuka K.; Tamatani T.;			
RT	"Cell surface molecule mediating cell adhesion and signal			
RT	transmission.";			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB023135; BAA62129.1; -			
KW	Signal.			
FT	SIGNAL.			
FT	SEQUENCE 199 AA; 22624 MW; 214EC741C9BDC9FC CRC64;			
FT	POTENTIAL.			

Query Match 76.8%; Score 152; DB 4; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.4e-156;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MMSGLWFFFLFCLRIKRVLTGELNGSANTYEMFFHNAGVQIILCKRYDYIQOQFMOLKGGQ 60
DB	1	MMSGLWFFFLFCLRIKRVLTGELNGSANTYEMFFHNAGVQIILCKRYDYIQOQFMOLKGGQ 60
OY	61	IICDILTKRGSGNTYSIKSLKFCQSOLSNNSVSPFLYNLDHSHAVYFCNLSIFPPPPPK 120
DB	61	IICDILTKRGSGNTYSIKSLKFCQSOLSNNSVSPFLYNLDHSHAVYFCNLSIFPPPPPK 120
OY	121	VLTGGLHYLHYESQLCCQLKFWLPITGCAFAVY 152
DB	121	VLTGGLHYLHYESQLCCQLKFWLPITGCAFAVY 152

RESULT 2  
Q9J1T7 PRELIMINARY; PRT; 200 AA.  
ID Q9J1T7  
AC Q9J1T7  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM PRECURSOR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tezuka K., Tamatani T.;  
RT "Cell surface molecule mediating cell adhesion and signal transmission."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB023134; BAA82128.1; -  
KW SIGNAL.  
FT SIGNAL.  
SQ SEQUENCE 200 AA; 22529 MW; 0A74C3581F129D4 CRC64;

Query Match 8.6%; Score 17; DB 11; Length 200;  
Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LCDLTKKSGGNTVSIK 78  
Db 62 LCDLTKKSGGNTVSIK 78

RESULT 3  
Q9WVR9 PRELIMINARY; PRT; 216 AA.  
ID Q9WVR9  
AC Q9WVR9  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM PRECURSOR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Tezuka K., Tamatani T.;  
RT "Cell surface molecule mediating cell adhesion and signal transmission."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB023133; BAA82127.1; -  
KW SIGNAL.  
FT SIGNAL.  
SQ SEQUENCE 216 AA; 24260 MW; 772E01320982B15A CRC64;

Query Match 8.6%; Score 17; DB 11; Length 216;  
Best Local Similarity 100.0%; Pred. No. 3e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LCDLTKKSGGNTVSIK 78  
Db 62 LCDLTKKSGGNTVSIK 78

RESULT 4  
Q9WVS0 PRELIMINARY; PRT; 200 AA.  
ID Q9WVS0

Q9WVS0;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).  
GN CCPLP OR ICOS.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Tezuka K., Tamatani T.;  
RT "Cell surface molecule mediating cell adhesion and signal transmission."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=SPLEEN;  
RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,  
RT "CCPLP, A novel molecule that regulates T cell activation."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=SPLEEN;  
RA Mages H.W., Hurlhoff A., Heuck C., Buchner K., Himmelbauer H.,  
RT "Molecular cloning and characterization of murine ICOS and identification of B7 as ICOS ligand."  
RL Eur. J. Immunol. 30:1040-1047(2000).  
DR EMBL; AB023132; BAA82126.1; -  
DR EMBL; AF257230; AAF70099.1; -  
DR EMBL; AJ250559; CAB71153.1; -  
KW SIGNAL.  
FT SIGNAL.  
SQ SEQUENCE 200 AA; 22690 MW; 9B2278E4CAB1DB47 CRC64;

Query Match 8.1%; Score 16; DB 11; Length 200;  
Best Local Similarity 100.0%; Pred. No. 3.4e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLHYESQLCCOLK 140  
Db 126 GGYLHYESQLCCOLK 141

RESULT 5  
Q9J1I7 PRELIMINARY; PRT; 200 AA.  
ID Q9J1I7  
AC Q9J1I7  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE CD28-RELATED PROTEIN 1 (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=INTESTINAL INTRA-EPITHELIUM;  
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Samlento U., Guo J.,  
RA Horan T., Shih G., Zhang M., Cocchia M.A., Kohno T., Tafuri-Bladt A.,  
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,  
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,  
RA Senaldi G.;  
RT "T-cell co-stimulation through B7RP-1 and ICOS."  
RL Nature 0:0-0(2000)  
DR EMBL; AF216748; AAF45150.1; -

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:04 ; Search time 12.96 Seconds  
(without alignments)  
293.499 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198

Sequence: 1 MKSGLMYFFLCRLIKVLG.....YMFMAVNTAKKRLFDVTL 198

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 0

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles!.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	3.0	8	1 US-08-480-505-4	Sequence 4, Appli
2	6	3.0	9	1 US-08-480-505-5	Sequence 5, Appli
3	6	3.0	9	1 US-08-480-505-8	Sequence 8, Appli
4	6	3.0	10	1 US-08-480-505-6	Sequence 6, Appli
5	6	3.0	10	1 US-08-446-692-79	Sequence 79, Appli
6	6	3.0	10	2 US-08-244-496-79	Sequence 79, Appli
7	6	3.0	10	2 US-08-488-351A-79	Sequence 79, Appli
8	6	3.0	10	2 US-08-817-933A-2	Sequence 2, Appli
9	6	3.0	11	1 US-08-480-505-1	Sequence 1, Appli
10	6	3.0	12	1 US-08-480-505-7	Sequence 7, Appli
11	6	3.0	30	2 US-08-408-858A-8	Sequence 8, Appli
12	6	3.0	45	1 US-08-446-692-103	Sequence 103, Appli
13	6	3.0	45	1 US-08-446-692-104	Sequence 104, Appli
14	6	3.0	45	2 US-08-488-351A-103	Sequence 103, Appli
15	6	3.0	45	2 US-08-488-351A-104	Sequence 104, Appli
16	6	3.0	65	3 US-08-331-625A-39	Sequence 39, Appli
17	6	3.0	108	6 5284931-5	Patent No. 5284931
18	6	3.0	109	1 US-08-037-579A-2	Sequence 2, Appli
19	6	3.0	109	3 US-08-601-184-2	Sequence 2, Appli
20	6	3.0	110	1 US-08-399-106A-6	Sequence 6, Appli
21	6	3.0	110	1 US-08-433-105A-6	Sequence 6, Appli
22	6	3.0	110	2 US-08-434-869A-6	Sequence 6, Appli
23	6	3.0	178	4 US-09-147-928-4	Sequence 4, Appli
24	6	3.0	194	2 US-08-272-255-20	Sequence 20, Appli
25	6	3.0	194	5 PCT-US95-08565-20	Sequence 20, Appli
26	6	3.0	203	3 US-08-331-625A-11	Sequence 11, Appli
27	6	3.0	235	1 US-08-015-986A-13	Sequence 13, Appli

28 6 3.0 235 2 US-08-446-363-13 Sequence 13, Appli  
29 6 3.0 318 6 5242798-5 Patent No. 5242798  
30 6 3.0 327 1 US-08-118-270-29 Sequence 29, Appli  
31 6 3.0 327 5 PCT-US93-08528-29 Sequence 29, Appli  
32 6 3.0 332 3 US-09-183-253-4 Sequence 4, Appli  
33 6 3.0 358 1 US-08-453-117-4 Sequence 4, Appli  
34 6 3.0 358 2 US-08-948-222-4 Sequence 4, Appli  
35 6 3.0 358 2 US-08-973-145-4 Sequence 4, Appli  
36 6 3.0 358 5 PCT-US96-08081-4 Sequence 5, Appli  
37 6 3.0 375 1 US-08-370-542-5 Sequence 5, Appli  
38 6 3.0 375 3 US-09-018-351-5 Sequence 5, Appli  
39 6 3.0 375 3 US-08-542-358-5 Sequence 5, Appli  
40 6 3.0 376 1 US-07-817-920-5 Sequence 5, Appli  
41 6 3.0 376 1 US-08-117-006-5 Sequence 5, Appli  
42 6 3.0 376 1 US-08-216-594-5 Sequence 5, Appli  
43 6 3.0 376 5 PCT-US93-00149-5 Sequence 5, Appli  
44 6 3.0 377 2 US-08-461-812-2 Sequence 2, Appli  
45 6 3.0 377 2 US-08-157-185-14 Sequence 14, Appli

#### ALIGNMENTS

RESULT 1  
US-08-480-505-4  
; Sequence 4, Application US/08480505  
; Patent No. 5601821  
; GENERAL INFORMATION:  
; APPLICANT: STANWORTH, DENIS R  
; APPLICANT: LEWIN, IAN V  
; APPLICANT: NAYYAR, SARITA  
; APPLICANT: JONES, VALERIE  
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND  
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22201-3360  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/480,505  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/102,692  
; FILING DATE:  
; APPLICATION NUMBER: US 07/776,380  
; FILING DATE: 26-NOV-1991  
; APPLICATION NUMBER: GB 8913737.6  
; FILING DATE: 15-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB90/00926  
; FILING DATE: 15-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MITCHARD, LEONARD C  
; REGISTRATION NUMBER: 29,009  
; REFERENCE/DOCKET NUMBER: 604-176  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 875-0400  
; TELEFAX: (703) 525-3468  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
US-08-480-505-4

Query Match 3.0%; Score 6; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 KTKGSG 72  
Db 1 KTKGSG 6

## RESULT 2

US-08-480-505-5  
; Sequence 5, Application US/08480505  
; Patent No. 5601821  
; GENERAL INFORMATION:  
; APPLICANT: STANWORTH, DENIS R  
; APPLICANT: LEWIN, IAN V  
; APPLICANT: NAYAR, SARITA  
; APPLICANT: JONES, VALERIE  
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND  
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22201-3360

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,505  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,692  
FILING DATE:  
APPLICATION NUMBER: US 07/776,380  
FILING DATE: 26-NOV-1991  
APPLICATION NUMBER: GB 8913737.6  
FILING DATE: 15-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB90/00926  
FILING DATE: 15-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHARD, LEONARD C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-176  
TELEPHONE: (703) 875-0400  
TELEFAX: (703) 525-3468  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-480-505-5

Query Match 3.0%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 KTKGSG 72  
Db 2 KTKGSG 7

## RESULT 3

US-08-480-505-8  
; Sequence 8, Application US/08480505  
; Patent No. 5601821  
; GENERAL INFORMATION:  
; APPLICANT: STANWORTH, DENIS R  
; APPLICANT: LEWIN, IAN V  
; APPLICANT: NAYAR, SARITA  
; APPLICANT: JONES, VALERIE  
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND  
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22201-3360  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,505  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,692  
FILING DATE:  
APPLICATION NUMBER: US 07/776,380  
FILING DATE: 26-NOV-1991  
APPLICATION NUMBER: GB 8913737.6  
FILING DATE: 15-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB90/00926  
FILING DATE: 15-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHARD, LEONARD C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-176  
TELEPHONE: (703) 875-0400  
TELEFAX: (703) 525-3468  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-480-505-8

Query Match 3.0%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 KTKGSG 72  
Db 1 KTKGSG 6

## RESULT 4